

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 06:56:31 ; Search time 190.191 Seconds
(without alignments)
2744.464 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319

Sequence: 1 gaaatgcgataagtaatgt.....ggaataccgctgaacttaa 319

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818139359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

1: /cgn2_6/prodata/1/ina/SA COMB.seq.*

2: /cgn2_6/prodata/1/ina/SB COMB.seq.*

3: /cgn2_6/prodata/1/ina/6A COMB.seq.*

4: /cgn2_6/prodata/1/ina/6B COMB.seq.*

5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq.*

6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	319	100.0	319	US-09-423-233-6	Sequence 6, Appli
2	244.4	76.6	2293	US-09-645-073-1	Sequence 1, Appli
3	240.2	75.3	310	US-09-423-233-7	Sequence 7, Appli
4	240	75.2	561	US-08-905-314A-24	Sequence 24, Appli
5	211	66.1	581	US-08-652-127C-6	Sequence 6, Appli
6	210	65.8	531	US-08-652-127C-7	Sequence 7, Appli
7	209.6	65.7	583	US-08-652-127C-8	Sequence 8, Appli
8	191.6	60.1	594	US-08-652-127C-5	Sequence 5, Appli
9	183.8	57.6	504	US-08-887-480-82	Sequence 82, Appli
10	183.8	57.6	504	US-08-905-314A-19	Sequence 19, Appli
11	183.8	57.6	504	US-08-722-187-82	Sequence 82, Appli
12	183.8	57.6	504	PCT-US95-04712-82	Sequence 82, Appli
13	180.4	56.6	545	US-08-887-480-84	Sequence 84, Appli
14	180.4	56.6	545	US-08-905-314A-21	Sequence 21, Appli
15	180	56.4	546	US-08-887-480-96	Sequence 96, Appli
16	180	56.4	546	US-08-905-314A-22	Sequence 22, Appli
17	174.8	54.8	503	US-08-887-480-83	Sequence 83, Appli
18	174.8	54.8	503	US-08-905-314A-20	Sequence 20, Appli
19	174.8	54.8	503	US-08-722-187-83	Sequence 83, Appli
20	174.8	54.8	503	PCT-US95-04712-83	Sequence 83, Appli
21	171.4	53.7	504	US-09-481-293-32	Sequence 32, Appli
22	156.8	49.2	611	US-08-986-727-4	Sequence 4, Appli
23	154.8	48.5	545	US-08-722-187-85	Sequence 85, Appli
24	154.8	48.5	545	PCT-US95-04712-85	Sequence 85, Appli
25	145.6	45.6	608	US-08-986-727-3	Sequence 3, Appli
26	128.4	40.3	605	US-08-986-727-1	Sequence 1, Appli
27	126.6	39.7	365	US-09-423-233-3	Sequence 3, Appli

28	125.8	39.4	617	3	US-08-986-727-2	Sequence 2, Appli
29	125	39.2	587	1	US-08-742-023-7	Sequence 7, Appli
30	125	39.2	587	1	US-08-968-505-7	Sequence 7, Appli
31	123.2	38.6	365	3	US-09-423-233-5	Sequence 5, Appli
32	121.2	38.0	364	3	US-09-423-233-2	Sequence 2, Appli
33	118	37.0	353	2	US-08-722-187-84	Sequence 84, Appli
34	118	37.0	353	5	PCT-US95-04712-84	Sequence 84, Appli
35	118	37.0	568	3	US-08-986-727-5	Sequence 5, Appli
36	115.8	36.3	556	1	US-08-887-480-85	Sequence 85, Appli
37	115.8	36.3	556	1	US-08-905-314A-23	Sequence 23, Appli
38	112.4	35.2	597	1	US-08-742-023-3	Sequence 3, Appli
39	112.4	35.2	597	1	US-08-968-505-3	Sequence 3, Appli
40	111.2	34.9	346	3	US-09-423-233-24	Sequence 24, Appli
41	111	34.8	526	4	US-09-481-293-33	Sequence 33, Appli
42	110.2	34.5	343	3	US-09-423-233-27	Sequence 27, Appli
43	110.2	34.5	344	3	US-09-423-233-26	Sequence 26, Appli
44	110.2	34.5	588	1	US-08-742-023-5	Sequence 5, Appli
45	110.2	34.5	588	3	US-08-968-505-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-423-233-6

; Sequence 6, Application US/09423233

; Patent No. 6372430

; GENERAL INFORMATION:

; APPLICANT: The Government of the United States of America as

; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and

; FILE REFERENCE: 03063-0341WP

; CURRENT APPLICATION NUMBER: US/09/423,233

; CURRENT FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 6

; LENGTH: 319

; TYPE: DNA

; ORGANISM: Fusarium solani

US-09-423-233-6

Query Match 100.0%; Score 319; DB 3; Length 319;
Best Local Similarity 100.0%; Pred. No. 3.2e-96;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAAATGCGATAGTAATGTAATTCAGTAATTCAGTAATTCATCGAATCTTTGAACGCA	60
Db	1	GAAATGCGATAGTAATGTAATTCAGTAATTCAGTAATTCATCGAATCTTTGAACGCA	60
Qy	61	CATTGCGCGCGCAGTATTCTGGCGGCATGCTGTTGAGCGTCATTACAAACCTTCAGG	120
Db	61	CATTGCGCGCGCAGTATTCTGGCGGCATGCTGTTGAGCGTCATTACAAACCTTCAGG	120
Qy	121	CCCCCGGCGCTGGCGTTCGGGATCGCGAAGCCCTTCGGGCAACAGCCGTCCTCCCA	180
Db	121	CCCCCGGCGCTGGCGTTCGGGATCGCGAAGCCCTTCGGGCAACAGCCGTCCTCCCA	180
Qy	181	AATACAGTGGCGGTCCCGCGCAGCTTCATTGCGTAGTAGTACACCTCGCAACTGGA	240
Db	181	AATACAGTGGCGGTCCCGCGCAGCTTCATTGCGTAGTAGTACACCTCGCAACTGGA	240
Qy	241	GAGCGCGCGGCGCAGCGCTGTAACCAACCACTTCTGAATGTTGACCTCGAATCAGGTAG	300
Db	241	GAGCGCGCGGCGCAGCGCTGTAACCAACCACTTCTGAATGTTGACCTCGAATCAGGTAG	300
Qy	301	GAATACCGCTGAACCTTAA	319
Db	301	GAATACCGCTGAACCTTAA	319

RESULT 2

US-09-645-073-1

OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 182..338
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 339..504
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 505..561
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-24

Query Match 75.2%; Score 240; DB 1; Length 561;
Best Local Similarity 88.7%; Pred. No. 8e-70;
Matches 282; Conservative 2; Mismatches 27; Indels 7; Gaps 2;

QY 2 AAATCGGATAAGTAATGTAATTCGAGGATTCAGTGAATTCATCGAATCTTTGAACGCAC 61
DB 231 AAATCGGATAAGTAATGTAATTCGAGGATTCAGTGAATTCATCGAATCTTTGAACGCAC 290

QY 62 ATTGCGCCGCCAGTATTCGCGGGGATCGCTGTTTCGAGCGTCAATACACCTCAGGC 121
DB 291 ATTGCGCCGCCAGTATTCGCGGGGATCGCTGTTTCGAGCGTCAATACACCTCAGGC 350

QY 122 CCCCGGCGCTGGGTTGGGATCGCGGAGCGCCCTCGGGGACACACCGCTCCGCCAA 181
DB 351 CCCCGGCGCTGGGTTGGGATCGCGGAGCGCCCTCGGGGACACACCGCTCCGCCAA 404

QY 182 ATACAGTGGCGGTCCCGCGGAGCTTCATTTGGTAGTAGTAAACACCTCGCAACTGGAG 241
DB 405 ATACATGGCGGTCTCGCTGCAGCTCCATTTGGTAGTAGTAAACACCTCGCAACTGGAG 464

QY 242 AGCGGCGCGCCACGCGGTAACAAACACCAACTTCTGAATGTTGAACCTCGAATCAGGTAGG 301
DB 465 CGCGGCGCGCCATGCGGTAACAAAC-CCCAACTTCTGAATGTTGAACCTCGAATCAGGTAGG 523

QY 302 AATACCCGCTGAACCTAA 319
DB 524 AATACCCGCTGAACCTAA 541

RESULT 5
US-08-652-127C-6
Sequence 6, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
ADDRESS: Seaby & MacLean
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034

REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 581
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-6

Query Match 66.1%; Score 211; DB 1; Length 581;
Best Local Similarity 85.5%; Pred. No. 3.7e-60;
Matches 272; Conservative 0; Mismatches 36; Indels 10; Gaps 3;

QY 3 AAATCGGATAAGTAATGTAATTCGAGGATTCAGTGAATTCATCGAATCTTTGAACGCAC 62
DB 253 AAATCGGATAAGTAATGTAATTCGAGGATTCAGTGAATTCATCGAATCTTTGAACGCAC 312

QY 63 TTGCGCCGCCAGTATTCGCGGGGATCGCTGTTTCGAGCGTCAATACACCTCAGGCC 122
DB 313 TTGCGCCGCCAGTATTCGCGGGGATCGCTGTTTCGAGCGTCAATACACCTCAGGCC 372

QY 123 CCCGGGCGTGGGTTGGGATCGCGGGAAGCGCCCTCGCGGACACACCGCGTCCCCCAA 182
DB 373 CCCGGGCGTGGGTTGGGATCGCGGGAAGCGCCCTCGCGGACACACCGCGTCCCCCAA 426

QY 183 TACAGTGGCGGTCCCGCGGAGCTTCATTTGGTAGTAGTAAACACCTCGCAACTGGAG 242
DB 427 TATAGTGGCGGTCTCGCTGTAGTCTTCTCTGCGTAGTAGACACCTCGC---ACTGGAA 483

QY 243 GCGGCGCGGCCACGCGGTAACAAACACCCAACTTCTG-AATGTTGACCTCGAATCAGGTAGG 301
DB 484 ACAGCGTGGCCACGCGGTAACAAACCCCACTTCTGAAAGTTGACCTCGAATCAGGTAGG 543

QY 302 AATACCCGCTGAACCTAA 319
DB 544 AATACCCGCTGAACCTAA 561

RESULT 6
US-08-652-127C-7
Sequence 7, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
ADDRESS: Seaby & MacLean
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: C0C 1944
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium culmorum
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
INDIVIDUAL ISOLATE: (consensus sequence)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..12
OTHER INFORMATION: /note= "3' end of small subunit"
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 13..161
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 162..318
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 319..472
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc feature
LOCATION: 473..504
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-19

Query Match 57.6%; Score 183.8; DB 1; Length 504;
Best Local Similarity 81.5%; Pred. No. 3.9e-51;
Matches 255; Conservative 1; Mismatches 38; Indels 19; Gaps 3;
Qy 2 AAATGCGATAAGTAATGTAATTCGAGAAATTCAGTGAATTCATCGAATCTTTGAACGCAC 61
Db 211 AAATGCGATAAGTAATGTAATTCGAGAAATTCAGTGAATTCATCGAATCTTTGAACGCAC 270
Qy 62 ATTGCGCCCGCCAGTATTCGCGGGCATGCTGTTTCGAGCGTCATTACACCTCAGGC 121
Db 271 ATTGCGCCCGCCAGTATTCGCGGGCATGCTGTTTCGAGCGTCATTACACCTCAGGC 330
Qy 122 CCCGGGCGCTGGCGTTGGGATCGGGGAAGCCCTCGCGGCACACGCCGTCGCCCAA 181
Db 331 CC---AGCTTGGTGTGGGAGCTG-----CAGTCCTGCTGCATCTCCCAA 372
Qy 182 ATACAGTGGCGGTCCCGCCGAGCTTCATTGGGTAGTAGCTAACACCTCGCAACTGGAG 241
Db 373 ATACATTGGCGGTCACTGTCAGCTTCATAGGCGTAGTAATTTACATATCTGTACTGGTA 432
Qy 242 AGCGGCGCGGCACCGCCGTAACACCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG 301
Db 433 ATCGTCGCGGCYACGCGGTGTTAAAC-CCCAACTTCTGAATGTTGACCTCGGATCAGGTAGG 491

Qy 302 AATACCCGCTGAA 314
Db 492 AATACCCGCTGAA 504
RESULT 11
US-08-722-187-82
Sequence 82, Application US/08722187
Patent No. 5955274
GENERAL INFORMATION:
APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum"
OTHER INFORMATION: (fculm.con)"
US-08-722-187-82

Query Match 57.6%; Score 183.8; DB 2; Length 504;
Best Local Similarity 81.5%; Pred. No. 3.9e-51;
Matches 255; Conservative 1; Mismatches 38; Indels 19; Gaps 3;
Qy 2 AAATGCGATAAGTAATGTAATTCGAGAAATTCAGTGAATTCATCGAATCTTTGAACGCAC 61
Db 211 AAATGCGATAAGTAATGTAATTCGAGAAATTCAGTGAATTCATCGAATCTTTGAACGCAC 270
Qy 62 ATTGCGCCCGCCAGTATTCGCGGGCATGCTGTTTCGAGCGTCATTACACCTCAGGC 121
Db 271 ATTGCGCCCGCCAGTATTCGCGGGCATGCTGTTTCGAGCGTCATTACACCTCAGGC 330
Qy 122 CCCGGGCGCTGGCGTTGGGATCGGGGAAGCCCTCGCGGCACACGCCGTCGCCCAA 181
Db 331 CC---AGCTTGGTGTGGGAGCTG-----CAGTCCTGCTGCATCTCCCAA 372

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QY 182 ATACAGTGGGGTCCCGCGCAGCTTCCATTGCGTAGTAGTAACACCTCGCAACTGGAG 241
Db 373 ATACATTGGGGTTCAGCTCGRAGCTTCCATAGCGTAGTAATTTACATATCGTTACTGGTA 432
QY 242 AGCGGCGCGCCACGCGGTAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG 301
Db 433 ATCGTCCGCGTACGCGGTTAAAC-CCCAACTTCTGAATGTTGACCTCGGATCAGGTAGG 491
QY 302 AATACCCGCTGAA 314
Db 492 AATACCCGCTGAA 504

RESULT 12
PCT-US95-04712-82
; Sequence 82, Application PC/TUS9504712
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,608
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Walsh, Andrea C.
; REGISTRATION NUMBER: 34,988
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8666
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..504
; OTHER INFORMATION: /note= "DNA sequence for the
; OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
; OTHER INFORMATION: (fculm.con)"
PCT-US95-04712-82

Query Match 57.6%; Score 183.8; DB 5; Length 504;
Best Local Similarity 81.5%; Pred. No. 3.9e-51;
Matches 255; Conservative 1; Mismatches 38; Indels 19; Gaps 3;

QY 2 AAAATGCGATAAGTGAATTCAGAGATTCAGTGAATCATCGAATCTTTGAACGCAC 61
Db 211 AAAATGCGATAAGTGAATTCAGAGATTCAGTGAATCATCGAATCTTTGAACGCAC 270
QY 62 ATTGCGCCCGCAGTATTCTGCGGGCGCATGCTGTTGCGAGCGTCATTACAACCTTCAGGC 121
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Db 271 ATTGCGCCCGCAGTATTCTGCGGGCGCATGCTGTTGCGAGCGTCATTCAACCCCTCAAGC 330
QY 122 CCCCGGCGCTGCGCTTGGGGATCGCGGGAAGCCCTCGGGGCAACAACCGCTCCCCCAA 181
Db 331 CC---AGCTTGGTGTGGAGCTG-----CAGTCTGCTGCACTCCCCCAA 372
QY 182 ATACAGTGGCGGTCCCGCGCAGCTTCCATTGCGTAGTAGTAACACCTCGCAACTGGAG 241
Db 373 ATACATTGGCGGTACAGTCGRAGCTTCCATAGCGTAGTAATTTACATATCGTTACTGGTA 432
QY 242 AGCGGCGCGCCACGCGGTAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG 301
Db 433 ATCGTCCGCGGACGCGGTTAAAC-CCCAACTTCTGAATGTTGACCTCGGATCAGGTAGG 491
QY 302 AATACCCGCTGAA 314
Db 492 AATACCCGCTGAA 504

RESULT 13
US-08-887-480-84
; Sequence 84, Application US/08887480
; Patent No. 581453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 581453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 545 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Fusarium moniliforme
; INDIVIDUAL ISOLATE: 4551
; IMMEDIATE SOURCE:
; CLONE: pCRFMON1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /note= "3' end of small subunit
; OTHER INFORMATION: rRNA gene"
; FEATURE:
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	NAME: Meigs, J. Timothy	
	REGISTRATION NUMBER: 38,241	
	REFERENCE/DOCKET NUMBER: CGC 1944	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: (919) 541-8587	
	TELEFAX: (919) 541-8689	
	INFORMATION FOR SEQ ID NO: 21:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 545 base pairs	
	TYPE: nucleic acid	
	STRANDEDNESS: single	
	TOPOLOGY: linear	
	MOLECULE TYPE: DNA (genomic)	
	ORGANISM: Fusarium moniliforme	
	INDIVIDUAL ISOLATE: 4551	
	IMMEDIATE SOURCE:	
	CLONE: PCRPMONI	
	FEATURE:	
	NAME/KEY: misc feature	
	LOCATION: 1..30	
	OTHER INFORMATION: /note= "3' end of small subunit"	
	OTHER INFORMATION: rRNA gene"	
	FEATURE:	
	NAME/KEY: misc feature	
	LOCATION: 31..178	
	OTHER INFORMATION: /note= "ITS 1"	
	FEATURE:	
	NAME/KEY: misc feature	
	LOCATION: 179..335	
	OTHER INFORMATION: /note= "5.8S rRNA gene"	
	OTHER INFORMATION: rRNA gene"	
	FEATURE:	
	NAME/KEY: misc feature	
	LOCATION: 336..488	
	OTHER INFORMATION: /note= "ITS 2"	
	FEATURE:	
	NAME/KEY: misc feature	
	LOCATION: 489..545	
	OTHER INFORMATION: /note= "5' end of large subunit"	
	OTHER INFORMATION: rRNA gene"	
	US-08-905-314A-21	
	Query Match	56.6%; Score 180.4; DB 1; Length 545;
	Best Local Similarity	82.4%; Pred. No. 5.5e-50;
	Matches 262; Conservative	0; Mismatches 36; Indels 20; Gaps 4;
QY	2 AAAATGCGATAAGTAATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTTGAACGCAC	61
DB	228 AAAATGCGATAAGTAATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTTGAACGCAC	287
QY	62 ATTGGCCGCCGAGTATTCGCGGGCATGCTGTCGAGCGTCATTACAACCCTCAGGC	121
DB	288 ATTGGCCGCCGAGTATTCGCGGGCATGCTGTCGAGCGTCATTACAACCCTCAGGC	347
QY	122 CCCCGGGCTGGCGTTGGGATCGCGGAAGCCCCCTCGCGGCACAAACGCCCTCCCACCA	181
DB	348 CC---AGCTTGTTGGAGCTG-----CAGTCTGCTGCATCTCCCAA	389
QY	182 ATACAGTGGCGTCCCGCCGAGTTTCCATTCGCTAGTAGTAACTCGAACCTGGAG	241
DB	390 ATACATTGGCGGTCAAGTCG-AGCTTCATAGCGTAGTAATTTACACATCGTTACTGGTA	448
QY	242 AGCGCGGGCCAGCCCGGTAAAACACCCCACTTCTGAATGTTGACCTCGAATCAGGTAGG	301
DB	449 ATCGTCGGCGGCACGCGTTAAAC-CCCACTTCTGAATGTTGACCTCGGATCAGGTAGG	507
QY	302 AATACCCGCTGAACTTAA	319
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	US-08-887-480-96	

Sequence 96, Application US/08887480
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Fusarium poae
INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus
INDIVIDUAL ISOLATE: sequence)
IMMEDIATE SOURCE:
CLONE: PCRfpoaeT427(1-2), PCRfpoaeT534(2-2), and
CLONE: PCRfpoaeT756(3-1)
FEATURE:
NAME/KEY: misc
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc
LOCATION: 31..180
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc
LOCATION: 181..337
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc
LOCATION: 338..489
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc
LOCATION: 490..546
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"

Query Match 56.4%; Score 180; DB 1; Length 546;
Best Local Similarity 82.4%; Pred. No. 7.5e-50;

Matches 262; Conservative 0; Mismatches 35; Indels 21; Gaps 4;
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Db |||||
Qy 230 AAAATGCCGATAGTAATGTGAATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCAC 289
Db |||||
Qy 62 ATTGCGCGCGCAGTATTCTGCGGGGCATGCTGTTGAGCGTCAATTACAACCCCTCAGGC 121
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Qy 290 ATTGCGCGCGCAGTATTCTGCGGGGCATGCTGTTGAGCGTCAATTACAACCCCTCAGGC 349
Qy 122 CCCCAGGCTGCGCTTGGGGATCGGGGAGCCCTCGGGGCACACCGCGTCCCCAA 181
Db |||||
Qy 350 CC---AGCTTGGTGTGGG-----ATCTGTGTGCAAAACACAGTCCCCAA 390
Qy 182 ATACAGTGGCGGTCCCGCGCAGCTTCATTGCGTAGTAGCTAAACACCTCGCAACTGGAG 241
Db |||||
Qy 391 ATTGATTGGCGGTACGTGCG-AGCTTCATAGCGTAGTAATTTACACATCGTTACTGGTA 449
Qy 242 AGCGCGCGGGCCACGCCCGTAAACACCCAACTTCTGGAATGTTGACCTCGAATCAGGTAGG 301
Db |||||
Qy 450 ATCGTGGGGGCCACGCCCGTTAAAC-CCCAACTTCTGGAATGTTGACCTCGGATCAGGTAGG 508
Qy 302 AATACCCGCTGAACTTAA 319
Db |||||
Qy 509 AATACCCGCTGAACTTAA 526

Search completed: October 23, 2005, 16:07:05
Job time : 192.191 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 15:20:46 ; Search time 1379.23 Seconds
(without alignments)
1907.926 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319

Sequence: 1 gaaatgcataagtaatgt.....ggaataccgcgtgaacttaa 319

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9772231 seqs, 4124568258 residues

Total number of hits satisfying chosen parameters: 19544462

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA:*

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- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
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- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	319	100.0	319	15	US-10-046-955-6
2	259	81.2	552	21	US-10-829-661-5
3	259	81.2	552	21	US-10-672-300-5
4	240.4	75.4	534	10	US-09-961-755A-7
5	240.4	75.4	534	20	US-10-773-904-7
6	240.4	75.4	534	20	US-10-773-905-7
7	240.2	75.3	310	15	US-10-046-955-7
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					Sequence 5, Appli
					Sequence 5, Appli
					Sequence 7, Appli
					Sequence 7, Appli
					Sequence 7, Appli

8	183.2	57.4	522	10	US-09-961-755A-5	Sequence 5, Appli
9	183.2	57.4	522	10	US-09-961-755A-8	Sequence 8, Appli
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12	183.2	57.4	522	20	US-10-773-905-5	Sequence 5, Appli
13	183.2	57.4	522	20	US-10-773-905-8	Sequence 8, Appli
14	176.4	55.3	521	10	US-09-961-755A-6	Sequence 6, Appli
15	176.4	55.3	521	20	US-10-773-904-6	Sequence 6, Appli
16	176.4	55.3	520	20	US-10-773-905-6	Sequence 6, Appli
17	169	53.0	780	20	US-10-425-115-137730	Sequence 137730,
18	131.8	41.3	652	16	US-10-121-740-2	Sequence 2, Appli
19	131.8	41.3	652	19	US-10-623-432-2	Sequence 2, Appli
20	131.8	41.3	652	24	US-11-131-659-2	Sequence 2, Appli
21	126.6	39.7	365	15	US-10-046-955-3	Sequence 3, Appli
22	126.4	39.6	577	22	US-10-757-093-28	Sequence 28, Appli
23	123.2	38.6	365	15	US-10-046-955-5	Sequence 5, Appli
24	121.2	38.0	364	15	US-10-046-955-2	Sequence 2, Appli
25	120	37.6	528	22	US-10-757-093-29	Sequence 29, Appli
26	119.8	37.6	650	16	US-10-121-740-4	Sequence 4, Appli
27	119.8	37.6	650	19	US-10-623-432-4	Sequence 4, Appli
28	119.8	37.6	650	24	US-11-131-659-4	Sequence 4, Appli
29	117.8	36.9	596	21	US-10-829-661-1	Sequence 1, Appli
30	117.8	36.9	596	21	US-10-672-300-1	Sequence 1, Appli
31	114.2	35.8	641	9	US-09-766-173C-4	Sequence 4, Appli
32	111.2	34.9	346	15	US-10-046-955-24	Sequence 24, Appli
33	110.6	34.7	618	9	US-09-766-173C-5	Sequence 5, Appli
34	110.2	34.5	343	15	US-10-046-955-27	Sequence 27, Appli
35	110.2	34.5	344	15	US-10-046-955-26	Sequence 26, Appli
36	109.2	34.2	346	15	US-10-046-955-25	Sequence 25, Appli
37	108	33.9	309	15	US-10-046-955-28	Sequence 28, Appli
38	107.2	33.6	466	17	US-10-356-320-1	Sequence 1, Appli
39	106.4	33.4	336	15	US-10-046-955-29	Sequence 29, Appli
40	105.6	33.1	377	9	US-09-961-663-14	Sequence 14, Appli
41	105.6	33.1	377	9	US-09-961-663-15	Sequence 15, Appli
42	105.6	33.1	377	9	US-09-961-663-16	Sequence 16, Appli
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44	103.6	32.5	495	21	US-10-829-661-6	Sequence 6, Appli
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ALIGNMENTS

RESULT 1

US-10-046-955-6
; Sequence 6, Application US/10046955
; Publication No. US20030129600A1

GENERAL INFORMATION:

; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for DI
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aldorevich, Liliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; TITLE OF INVENTION: Other Filamentous Fungi

; FILE REFERENCE: 6395-62064

; CURRENT APPLICATION NUMBER: US/10/046,955

; CURRENT FILING DATE: 2002-06-04

; PRIOR APPLICATION NUMBER: US 09/423,233

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: PCT/US98/08926

; PRIOR FILING DATE: 1998-05-01

; PRIOR APPLICATION NUMBER: US 60/045,400

; PRIOR FILING DATE: 1997-05-02

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 319

; TYPE: DNA

; ORGANISM: Fusarium solani

; US-10-046-955-6

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7

Query Match 75.4%; Score 240.4; DB 10; Length 534;
Best Local Similarity 87.9%; Pred. No. 6.8e-75;
Matches 276; Conservative 0; Mismatches 31; Indels 7; Gaps 1;

QY 2 AAATGCGTAAGTAATGGAATTCAGAAATTCAGTAATCATCGAATCTTTGAACGCAC 61
DB 228 AAATGCGTAAGTAATGGAATTCAGAAATTCAGTAATCATCGAATCTTTGAACGCAC 287

QY 62 ATTGCGCCGCCAGTATCTGCGGGCATGCTGTTTCGAGCGTCATTACAAACCTTCAGGC 121
DB 288 ATTGCGCCGCCAGTATCTGCGGGCATGCTGTTTCGAGCGTCATTACAAACCTTCAGGC 347

QY 122 CCCCGGCTTGGGATGCGGGAAGCCCTTCGCGGCACAAACCGCTCCGCCAA 181
DB 348 CCCCGGCTTGGGATGCGGGAAGCCCTTCGCGGCACAAACCGCTCCGCCAA 400

QY 182 ATACAGTGGCGTCCCGCGAGCTTCCATTGCGTAGTAGCTAAACACCTTCGCAACTGGAG 241
DB 401 ATCTAGTGGCGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAACACCTTCGCAACTGGTA 460

QY 242 AGCGGCGGCCAGCCGCTAAACACCACTTCTGAATGTTGACCTCGAATCAGGTAGG 301
DB 461 CGCGGCGGCCAGCCGCTAAACACCACTTCTGAATGTTGACCTCGAATCAGGTAGG 520

QY 302 AATACCCGCTGAAC 315
DB 521 AATACCCGCTGAAC 534

RESULT 5
US-10-773-904-7
; Sequence 7, Application US/10773904
; Publication No. US20040259120A1
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/10/773,904
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/09/961,755
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-10-773-904-7

Query Match 75.4%; Score 240.4; DB 20; Length 534;
Best Local Similarity 87.9%; Pred. No. 6.8e-75;
Matches 276; Conservative 0; Mismatches 31; Indels 7; Gaps 1;

QY 2 AAATGCGTAAGTAATGGAATTCAGAAATTCAGTAATCATCGAATCTTTGAACGCAC 61
DB 228 AAATGCGTAAGTAATGGAATTCAGAAATTCAGTAATCATCGAATCTTTGAACGCAC 287

QY 62 ATTGCGCCGCCAGTATCTGCGGGCATGCTGTTTCGAGCGTCATTACAAACCTTCAGGC 121
DB 288 ATTGCGCCGCCAGTATCTGCGGGCATGCTGTTTCGAGCGTCATTACAAACCTTCAGGC 347

QY 122 CCCCGGCTTGGGATGCGGGAAGCCCTTCGCGGCACAAACCGCTCCGCCAA 181
DB 348 CCCCGGCTTGGGATGCGGGAAGCCCTTCGCGGCACAAACCGCTCCGCCAA 400

QY 182 ATACAGTGGCGTCCCGCGAGCTTCCATTGCGTAGTAGCTAAACACCTTCGCAACTGGAG 241
DB 401 ATCTAGTGGCGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAACACCTTCGCAACTGGTA 460

QY 242 AGCGGCGGCCAGCCGCTAAACACCACTTCTGAATGTTGACCTCGAATCAGGTAGG 301
DB 461 CGCGGCGGCCAGCCGCTAAACACCACTTCTGAATGTTGACCTCGAATCAGGTAGG 520

QY 302 AATACCCGCTGAAC 315
DB 521 AATACCCGCTGAAC 534

Db 348 CCCCGGCTTGGGATGCGGGAAGCCCTTCGCGGC-----AAGCCGCCGCCGAA 400
QY 182 ATACAGTGGCGTCCCGCGAGCTTCCATTGCGTAGTAGCTAAACACCTTCGCAACTGGAG 241
Db 401 ATCTAGTGGCGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAACACCTTCGCAACTGGTA 460
QY 242 AGCGGCGGCCAGCCGCTAAACACCACTTCTGAATGTTGACCTCGAATCAGGTAGG 301
Db 461 CGCGGCGGCCAGCCGCTAAACACCACTTCTGAATGTTGACCTCGAATCAGGTAGG 520
QY 302 AATACCCGCTGAAC 315
Db 521 AATACCCGCTGAAC 534

RESULT 6
US-10-773-905-7
; Sequence 7, Application US/10773905
; Publication No. US20040259121A1
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/10/773,905
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/09/961,755
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-10-773-905-7

Query Match 75.4%; Score 240.4; DB 20; Length 534;
Best Local Similarity 87.9%; Pred. No. 6.8e-75;
Matches 276; Conservative 0; Mismatches 31; Indels 7; Gaps 1;

QY 2 AAATGCGTAAGTAATGGAATTCAGAAATTCAGTAATCATCGAATCTTTGAACGCAC 61
DB 228 AAATGCGTAAGTAATGGAATTCAGAAATTCAGTAATCATCGAATCTTTGAACGCAC 287

QY 62 ATTGCGCCGCCAGTATCTGCGGGCATGCTGTTTCGAGCGTCATTACAAACCTTCAGGC 121
DB 288 ATTGCGCCGCCAGTATCTGCGGGCATGCTGTTTCGAGCGTCATTACAAACCTTCAGGC 347

QY 122 CCCCGGCTTGGGATGCGGGAAGCCCTTCGCGGCACAAACCGCTCCGCCAA 181
DB 348 CCCCGGCTTGGGATGCGGGAAGCCCTTCGCGGCACAAACCGCTCCGCCAA 400

QY 182 ATACAGTGGCGTCCCGCGAGCTTCCATTGCGTAGTAGCTAAACACCTTCGCAACTGGAG 241
DB 401 ATCTAGTGGCGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAACACCTTCGCAACTGGTA 460

QY 242 AGCGGCGGCCAGCCGCTAAACACCACTTCTGAATGTTGACCTCGAATCAGGTAGG 301
DB 461 CGCGGCGGCCAGCCGCTAAACACCACTTCTGAATGTTGACCTCGAATCAGGTAGG 520

QY 302 AATACCCGCTGAAC 315
DB 521 AATACCCGCTGAAC 534

RESULT 7
US-10-046-955-7
; Sequence 7, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; SECRETARY: Secretary of the Department of Health and Human Services, Centers for Dis

```
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aldorevich, Lilliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; TITLE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
; ORGANISM: Fusarium moniliforme
US-10-046-955-7

Query Match 75.3%; Score 240.2; DB 15; Length 310;
Best Local Similarity 87.4%; Pred. No. 6.6e-75;
Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;

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Qy 63 TTGGCCCGCCAGATTTCTGGCGGGCATGCTTTCAGAGGTGATTAACACCCCTCAGGCC 122
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Db 121 CCCGGGTTGGTGTGGGGATCGCGGAAGCCCTTCGGGC-----AAGCCGGCCCCGAAA 173
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Qy 243 GCGGGCGGCGCACGCGGTAAACACCCAACTTCTGAAATGTTGACCTCGAATCAGGTAGGA 302
Db 234 GCGGGCGGCGCAAGCGGTAAACCCCAACTTCTGAAATGTTGACCTCGGATCAGGTAGGA 293
Qy 303 ATACCCGCTGAACCTTAA 319
Db 294 ATACCCGCTGAACCTTAA 310

RESULT 8
US-09-961-755A-5
; Sequence 5, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium subglutinans
US-09-961-755A-5

Query Match 75.4%; Score 183.2; DB 10; Length 522;
Best Local Similarity 83.4%; Pred. No. 1.8e-54;
Matches 262; Conservative 0; Mismatches 33; Indels 19; Gaps 4;

Qy 2 AAAATGCGATAAGTAATGTGAATTCAGAAATTCAGTGAATCATCGAAATCTTTTGAACGCAC 61
Db 228 AAAATGCGATAAGTAATGTGAATTCAGAAATTCAGTGAATCATCGAAATCTTTTGAACGCAC 287
Qy 62 ATTGCGCCCGCCAGTATTTCTGGCGGGCATGCTTTCGAGCGTCAATTACAACCCCTCAGGC 121
Db 288 ATTGCGCCCGCCAGTATTTCTGGCGGGCATGCTTTCGAGCGTCAATTACAACCCCTCAGGC 347
Qy 122 CCCGGGCTGGCTTGGGGATCGCGGAAGCCCTCGGGGCACAAACCGCTGCCCAAA 181
Db 348 CC---AGCTTGGTGTGGGACTC-----GCGAGTCAAAATCGCGTTCCCAAA 390
Qy 182 ATACAGTGGCGGTCCCGCCAGCTTCCATTGCGTAGTAGCTAAACACCTCGCAACTGGAG 241
Db 391 ATTGATTGGCGGTACGTCG-AGCTTCCATAGGTAGTAGTAAACACCTCGTTACTGGTA 449
Qy 242 AGCGGGCGGCGCACGCGGTAAACACCCAACTTCTGAAATGTTGACCTCGAATCAGGTAGG 301
Db 450 ATCGTCGCGGCCACGCGGTAAAC-CCCAACTTCTGAAATGTTGACCTCGGATCAGGTAGG 508

RESULT 9
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; Sequence 8, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
US-09-961-755A-8

Query Match 57.4%; Score 183.2; DB 10; Length 522;
Best Local Similarity 83.4%; Pred. No. 1.8e-54;
Matches 262; Conservative 0; Mismatches 33; Indels 19; Gaps 4;

Qy 2 AAAATGCGATAAGTAATGTGAATTCAGAAATTCAGTGAATCATCGAAATCTTTTGAACGCAC 61
Db 228 AAAATGCGATAAGTAATGTGAATTCAGAAATTCAGTGAATCATCGAAATCTTTTGAACGCAC 287
Qy 62 ATTGCGCCCGCCAGTATTTCTGGCGGGCATGCTTTCGAGCGTCAATTACAACCCCTCAGGC 121
Db 288 ATTGCGCCCGCCAGTATTTCTGGCGGGCATGCTTTCGAGCGTCAATTACAACCCCTCAGGC 347
Qy 122 CCCGGGCTGGCTTGGGGATCGCGGAAGCCCTCGGGGCACAAACCGCTGCCCAAA 181
Db 348 CC---AGCTTGGTGTGGGACTC-----GCGAGTCAAAATCGCGTTCCCAAA 390
Qy 182 ATACAGTGGCGGTCCCGCCAGCTTCCATTGCGTAGTAGCTAAACACCTCGCAACTGGAG 241
Db 391 ATTGATTGGCGGTACGTCG-AGCTTCCATAGGTAGTAGTAAACACCTCGTTACTGGTA 449
Qy 242 AGCGGGCGGCGCACGCGGTAAACACCCAACTTCTGAAATGTTGACCTCGAATCAGGTAGG 301
Db 450 ATCGTCGCGGCCACGCGGTAAAC-CCCAACTTCTGAAATGTTGACCTCGGATCAGGTAGG 508
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Qy 302 AATACCCGCTGAAC 315
Db 509 AATACCCGCTGAAC 522

RESULT 10
US-10-773-904-5
; Sequence 5, Application US/10773904
; Publication No. US20040259120A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/09/961,755
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium subglutinans
US-10-773-904-5

Query Match 57.4%; Score 183.2; DB 20; Length 522;
Best Local Similarity 83.4%; Pred. No. 1.8e-54;
Matches 262; Conservative 0; Mismatches 33; Indels 19; Gaps 4;

Qy 2 AAAATGCGATAAGTAATGGAATTCAGAGATTCAGTGAATCATCGAATCTTTTGAACGCAC 61
Db 228 AAAATGCGATAAGTAATGGAATTCAGAGATTCAGTGAATCATCGAATCTTTTGAACGCAC 287

Qy 62 ATTGCGCCCGCAGTATTCTGCGGGCATGCTGTTGAGCGCTGTTTCAACCCCTCAGGC 121
Db 288 ATTGCGCCCGCAGTATTCTGCGGGCATGCTGTTGAGCGCTGTTTCAACCCCTCAGGC 347

Qy 122 CCGCGGCGCTGCGGTTGGGATCGCGGAAGCCCTCGGGGCACACGCCCTGCCCAA 181
Db 348 CC---AGCTTGGTGTGGACTC-----GCGAGTCAAAATCGCGTTCCCAA 390

Qy 182 ATACAGTGGCGTCCCGCGCAGCTTCCATTGCGTAGTCTGCTGCACTCGCACTGGAG 241
Db 391 ATTGATTGCGGTCACTGCG-AGCTTCATAGCTAGTAGTAAACCCCTCGTTACTGGTA 449

Qy 242 AGCGGCGGCGCACGCCGTAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG 301
Db 450 ATCGTCGCGGCGCACGCCGTAAAC-CCCAACTTCTGAATGTTGACCTCGGATCAGGTAGG 508

Qy 302 AATACCCGCTGAAC 315
Db 509 AATACCCGCTGAAC 522

RESULT 11
US-10-773-904-8
; Sequence 8, Application US/10773904
; Publication No. US20040259120A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/09/961,755
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8

Query Match 57.4%; Score 183.2; DB 20; Length 522;
Best Local Similarity 83.4%; Pred. No. 1.8e-54;
Matches 262; Conservative 0; Mismatches 33; Indels 19; Gaps 4;

Qy 2 AAAATGCGATAAGTAATGGAATTCAGAGATTCAGTGAATCATCGAATCTTTTGAACGCAC 61
Db 228 AAAATGCGATAAGTAATGGAATTCAGAGATTCAGTGAATCATCGAATCTTTTGAACGCAC 287

Qy 62 ATTGCGCCCGCAGTATTCTGCGGGCATGCTGTTGAGCGCTGTTTCAACCCCTCAGGC 121
Db 288 ATTGCGCCCGCAGTATTCTGCGGGCATGCTGTTGAGCGCTGTTTCAACCCCTCAGGC 347

Qy 122 CCGCGGCGCTGCGGTTGGGATCGCGGAAGCCCTCGGGGCACACGCCCTGCCCAA 181
Db 348 CC---AGCTTGGTGTGGACTC-----GCGAGTCAAAATCGCGTTCCCAA 390

Qy 182 ATACAGTGGCGTCCCGCGCAGCTTCCATTGCGTAGTCTGCTGCACTCGCACTGGAG 241
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QY 122 CCCCCGGCCTGGCGTTGGGATCGGCGGAAGCCCCCTGCGGGGCACAAAGCCCGTCCCCCAA 181
Db 348 CC---AGCTTGGTGTGGGAGCTG-----CAGTCCTGCTGCACCTCCCAA 389
QY 182 ATACAGTGGCGTCCCGCCGAGCTTCCATTGGTAGTAGCTAACACCTCGCACTGGAG 241
Db 390 ATACATTGGCGGTACGTCG-AGCTTCCATAGCGTAGTAATTACACATCGTTACTGGTA 448
QY 242 AGCGCGCGGCCACGCGGTAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG 301
Db 449 ATCGTCGCGGCCACGCGGTAAAC-CCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG 507
QY 302 AATACCGCTGAAC 315
Db 508 AATACCGCTGAAC 521
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Search completed: October 23, 2005, 23:48:15
Job time : 1381.23 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 06:56:31 ; Search time 184.825 Seconds
(without alignments)
2744.464 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310

Sequence: 1 aatgcgataagtaagtga.....ggaataccgctgaactaa 310

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/prodata/1/ina/5B COMB.seq:*

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4: /cgn2_6/prodata/1/ina/6B COMB.seq:*

5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq:*

6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	310	100.0	310	3	US-09-423-233-7
2	306.8	99.0	2293	3	US-09-645-073-1
3	249.8	80.6	561	1	US-08-905-314A-24
4	240.2	77.5	319	3	US-09-423-233-6
5	231	74.5	583	1	US-08-652-127C-8
6	225.2	72.6	531	1	US-08-652-127C-7
7	224.2	72.3	581	1	US-08-652-127C-6
8	197.8	63.8	594	1	US-08-652-127C-5
9	187.6	60.5	546	1	US-08-887-480-96
10	187.6	60.5	546	1	US-08-905-314A-22
11	186.6	60.2	504	1	US-08-887-480-82
12	186.6	60.2	504	1	US-08-905-314A-19
13	186.6	60.2	504	2	US-08-722-187-82
14	186.6	60.2	504	5	PCT-US95-04712-82
15	185	59.7	611	3	US-08-986-727-4
16	183.2	59.1	545	1	US-08-887-480-84
17	183.2	59.1	545	1	US-08-905-314A-21
18	180.4	58.2	503	1	US-08-887-480-83
19	180.4	58.2	503	1	US-08-905-314A-20
20	180.4	58.2	503	2	US-08-722-187-83
21	180.4	58.2	503	5	PCT-US95-04712-83
22	174.2	56.2	504	4	US-09-481-293-32
23	166.2	53.6	545	2	US-08-722-187-85
24	166.2	53.6	545	5	PCT-US95-04712-85
25	163.8	52.8	608	3	US-08-986-727-3
26	139	44.8	605	3	US-08-986-727-1
27	136	43.9	365	3	US-09-423-233-3

28	136	43.9	587	1	US-08-742-023-7	Sequence 7, Appli
29	136	43.9	587	3	US-08-968-505-7	Sequence 7, Appli
30	136	43.9	617	3	US-08-986-727-2	Sequence 2, Appli
31	131.4	42.4	364	3	US-09-423-233-2	Sequence 2, Appli
32	126.6	40.8	556	3	US-09-037-990B-7	Sequence 7, Appli
33	125.2	40.4	627	1	US-08-233-608-47	Sequence 47, Appli
34	125.2	40.4	627	1	US-08-887-480-47	Sequence 47, Appli
35	125.2	40.4	627	2	US-08-722-187-47	Sequence 47, Appli
36	125.2	40.4	627	5	PCT-US95-04712-47	Sequence 47, Appli
37	125	40.3	309	3	US-09-423-233-28	Sequence 28, Appli
38	124.4	40.1	536	4	US-09-517-790-5	Sequence 5, Appli
39	124.4	40.1	556	1	US-08-887-480-85	Sequence 85, Appli
40	124.4	40.1	556	1	US-08-905-314A-23	Sequence 23, Appli
41	124.4	40.1	580	1	US-08-742-023-6	Sequence 6, Appli
42	124.4	40.1	580	3	US-08-968-505-6	Sequence 6, Appli
43	123.6	39.9	626	1	US-08-233-608-3	Sequence 3, Appli
44	123.6	39.9	626	1	US-08-887-480-3	Sequence 3, Appli
45	123.6	39.9	626	2	US-08-722-187-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-423-233-7

; Sequence 7, Application US/09423233

; Patent No. 6372430

; GENERAL INFORMATION:

; APPLICANT: The Government of the United States of America as

; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and

; FILE REFERENCE: 03063-0341WP

; CURRENT APPLICATION NUMBER: US/09/423,233

; CURRENT FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 7

; LENGTH: 310

; TYPE: DNA

; ORGANISM: Fusarium moniliforme

US-09-423-233-7

Query Match 100.0%; Score 310; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.7e-94;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AAATCGGATAGTAATCTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA	60
Db	1	AAATCGGATAGTAATCTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA	60
Qy	61	TTGCGCCCGCCAGTATCTCGGGGGCATGCGCTGTTTCGAGCGTCATTTCAACCCCTCAAGCC	120
Db	61	TTGCGCCCGCCAGTATCTCGGGGGCATGCGCTGTTTCGAGCGTCATTTCAACCCCTCAAGCC	120
Qy	121	CCCGGGTTGGTGTGGGGATCGGCAAGCCCTTCGCGGAAGCCGCCCGGCGGCGC	180
Db	121	CCCGGGTTGGTGTGGGGATCGGCAAGCCCTTCGCGGAAGCCGCCCGGCGGCGC	180
Qy	181	GGGCTCGCTCGACGCTTCATTCGCTAGTAGTAAACCTCGCACTGGTACGGCGCGC	240
Db	181	GGGCTCGCTCGACGCTTCATTCGCTAGTAGTAAACCTCGCACTGGTACGGCGCGC	240
Qy	241	GGCCAAAGCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCGG	300
Db	241	GGCCAAAGCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCGG	300
Qy	301	CTGAACCTTAA	310
Db	301	CTGAACCTTAA	310

RESULT 2

US-09-645-073-1

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; Sequence 1, Application US/09645073
; Patent No. 6287800
; GENERAL INFORMATION:
; APPLICANT: Lee, May
; TITLE OF INVENTION: Production of High Titrers of Gibberellins GA4 and GA7
; FILE REFERENCE: L02-01NP
; CURRENT APPLICATION NUMBER: US/09/645,073
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,770
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: Gibberella fujikuroi
US-09-645-073-1

Query Match      99.0%; Score 306.8; DB 3; Length 2293;
Best Local Similarity 99.4%; Pred. No. 1.6e-92;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  AAATGCGATAAGTAATGTAATTCGAAATTCAGTGAATCATCGAATCTTTTGAACGCACA 60
Db      1972 AAATGCGATAAGTAATGTAATTCGAAATTCAGTGAATCATCGAATCTTTTGAACGCACA 2031

Qy      61  TTGGCGCCGCCAGTATTCTTGGCGGGCATGCTTTCGAGCGTCAATTTCAACCCCTCAAGCC 120
Db      2032 TTGGCGCCGCCAGTATTCTTGGCGGGCATGCTTTCGAGCGTCAATTTCAACCCCTCAAGCC 2091

Qy      121 CCCGGGTTTGTTGGGATCGCAAGCCCTTTCGGGCAAGCCGCGCCCGGAAATCTAGTG 180
Db      2092 CCCGGGTTTGTTGGGATCGCGAGCCCTTTCGGGCAAGCCGCGCCCGGAAATCTAGTG 2151

Qy      181 GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAACCCCTCGCAACTGGTACGCGCGC 240
Db      2152 GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAACCCCTCGCAACTGGTACGCGCGC 2211

Qy      241 GGCCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGATCAGGTAGGAATACCCG 300
Db      2212 GGCCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGATCAGGTAGGAATACCCG 2271

Qy      301 CTGAACCTTAA 310
Db      2272 CTGAACCTTAA 2281

RESULT 3
US-08-905-314A-24
; Sequence 24, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827695artis Corporation Patent Department
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314A
; FILING DATE:
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Fusarium avenaceum
; INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /note= "3' end of small subunit"
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..181
; OTHER INFORMATION: /note= "ITS 1"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 182..338
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 339..504
; OTHER INFORMATION: /note= "ITS 2"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 505..561
; OTHER INFORMATION: /note= "5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
; US-08-905-314A-24

Query Match      80.6%; Score 249.8; DB 1; Length 561;
Best Local Similarity 91.6%; Pred. No. 1.1e-73;
Matches 285; Conservative 1; Mismatches 23; Indels 2; Gaps 2;

Qy      1  AAATGCGATAAGTAATGTGAATTCGAAATTCGAAATTCAGTGAATCATCGAATCTTTTGAACGCACA 60
Db      232 AAATGCGATAAGTAATGTGAATTCGAAATTCGAAATTCAGTGAATCATCGAATCTTTTGAACGCACA 291

Qy      61  TTGGCGCCGCCAGTATTCTTGGCGGGCATGCTTTCGAGCGTCAATTTCAACCCCTCAAGCC 120
Db      292 TTGGCGCCGCCAGTATTCTTGGCGGGCATGCTTTCGAGCGTCAATTTCAACCCCTCAAGCC 351

Qy      121 CCCGGGTTTGTTGGGATCGCAAGCCCTTTCGGC- AAGCGCGGCCCGGAAATCTAGT 179
Db      352 CCCGGGTTTGTTGGGATCGGCTCTGCTTMYGGCGTGGCGGCCCGGAAATACATT 411

Qy      180 GCGCGTCTCGCTCGAGCTTCATTGCGTAGTAGTAAACCCCTCGCAACTGGTACGCGGCG 239
Db      412 GCGCGTCTCGCTCGAGCTTCATTGCGTAGTAGTAAACCCCTCGCAACTGGAAACGCGGCG 471

Qy      240 CGGCCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGATCAGGTAGGAATACCC 299
Db      472 CGGCCAATGCGC- TAAACCCCAACTTCTGAATGTTGACCTCGATCAGGTAGGAATACCC 530

Qy      300 GCTGAACCTTAA 310
Db      531 GCTGAACCTTAA 541

RESULT 4
US-09-423-233-6
; Sequence 6, Application US/09423233
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; Patent No. 6372430
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341WP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
; US-09-423-233-6

Query Match      77.5%; Score 240.2; DB 3; Length 319;
Best Local Similarity 87.4%; Pred. No. 1.5e-70;
Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;

QY 1 AAATGCGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAAACGCACA 60
DB 3 AAATGCGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAAACGCACA 62
QY 61 TTGCGCCCGCCAGTATTCGCGGGGCGATGCGCTGTTGAGAGCGTCAATTCACACCTCAAGCC 120
DB 63 TTGCGCCCGCCAGTATTCGCGGGGCGATGCGCTGTTGAGAGCGTCAATTCACACCTCAAGCC 122
QY 121 CCCGGGTTTGGTGTGGGGATCGCAAGCCCTTGGCGC-----AAGCGGCGCCCGAAA 173
DB 123 CCCGGGCTGGCGTGGGGATCGCGGAGCCCGCTGCGGGGCAACAGCCGCTCCCCCAA 182
QY 174 TCTAGTGGCGGTCTCGTGCAGCTTCATTTGCGTAGTGTAGTAAACCTCGCAACTGGTAC 233
DB 183 TACAGTGGCGGTCCCGCGCGAGCTTCATTTGCGTAGTGTAGTAAACCTCGCAACTGGAGA 242
QY 234 GCGGCGGGCGCAAGCGTTAAACCCCACTTCTGAATGTTGACCTCGGATCAGGTAGGA 293
DB 243 GCGGCGGGCGCACGCGTTAAACACCACTTCTGAATGTTGACCTCGAATCAGGTAGGA 302
QY 294 ATACCCGCTGAACCTAA 310
DB 303 ATACCCGCTGAACCTAA 319

RESULT 5
US-08-652-127C-8
; Sequence 8, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; ADDRESSEE: Seaby & MacLean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
```

```
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-8

Query Match      74.5%; Score 231; DB 1; Length 583;
Best Local Similarity 90.4%; Pred. No. 2.3e-67;
Matches 281; Conservative 0; Mismatches 25; Indels 5; Gaps 3;

QY 1 AAATGCGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAAACGCACA 60
DB 257 AAATGCGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAAACGCACA 316
QY 61 TTGCGCCCGCCAGTATTCGCGGGGCGATGCGCTGTTGAGAGCGTCAATTCACACCTCAAGCC 120
DB 317 TTGCGCCCGCCAGTATTCGCGGGGCGATGCGCTGTTGAGAGCGTCAATTCACACCTCAAGCC 376
QY 121 CCCGGGTTTGGTGTGGGGATCGCAAGCCCTTGGGGCAAGCGCGCCCGCAAACTCTAGTG 180
DB 377 CCCGGGCTTGGTGTGGGGATCGCGAGCCTCCGC-GCCGCGCGCTCCCTAAATCTAGTG 435
QY 181 GCGGCTCGCTCAGCTTCCATTTGCGTAGTGTAGTAAACCTCGCAACTGGTACGCGCGC 240
DB 436 GCGGCTCGCTCAGCTTCCCTCTGGGTAGTACACACCTCGC---ACTGGGAAACAGCGC 492
QY 241 GCGCAAGCGGTAAACCCCAACTTCTGAATG-TTGACCTCGGATCAGGTAGGAATACCC 299
DB 493 GCGCACGCGTTAAACCCCAACTTCTGAAGTTTGACCTCGGATCAGGTAGGAATACCC 552
QY 300 GCTGAACCTAA 310
DB 553 GCTGAACCTAA 563

RESULT 6
US-08-652-127C-7
; Sequence 7, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; ADDRESSEE: Seaby & MacLean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-652-127C-7

Query Match      72.6%; Score 225.2; DB 1; Length 531;
Best Local Similarity 88.8%; Pred. No. 2e-65;
Matches 277; Conservative 0; Mismatches 30; Indels 5; Gaps 3;

QY 1 AAATGCGATAAGTAATGTAATTCAGAAATTCAGTAATCATCGAAATCTTTGAACGCACA 60
Db 203 AAATGCGATAAGTAATGTAATTCAGAAATTCAGTAATCATCGAAATCTTTGAACGCACA 262
QY 61 TTGGCGCCCGCCAGATATCTGGCGGCGCATGCGCTGTTGAGCGGTCAATTTCAACCCCTCAAGCC 120
Db 263 TTGGCGCCCGCCAGATATCTGGCGGCGCATGCGCTGTTGAGCGGTCAATTTCAACCCCTCAAGCC 322
QY 121 CCCGGGTTTGGTGTGGGATCGGCAAG-CCCTTGGCGGCAAGCCGCGCCCGCAAAATCTAGT 179
Db 323 CCCGGGTTTGGTGTGGGATCGGCAAG-CCCTTGGCGGCAAGCCGCGCCCGCAAAATCTAGT 382
QY 180 GGCGGTCTCGCTGAGCTTCCATTCGCTAGTAGTAAGAAACCTCGCAACTGGTACGCGCGC 239
Db 383 GGCGGTCTCGCTGAGCTTCCATTCGCTAGTAGTAAGAAACCTCGCAACTGGTACGCGCGC 439
QY 240 CGGCAAGCCGTTAAACCCCAACTTCTG-AAATGTTGACCTCGGATCAGGTAGGAATACC 298
Db 440 CGGCAAGCCGTTAAACCCCAACTTCTG-AAATGTTGACCTCGGATCAGGTAGGAATACC 499
QY 299 CGCTGAACCTTAA 310
Db 500 CGCTGAACCTTAA 511

RESULT 7
US-08-652-127C-6
; Sequence 6, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; ADDRESSEE: Seaby & MacLean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24, 034
; REFERENCE/DOCKET NUMBER: 1898
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-652-127C-5

; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-652-127C-6

Query Match      72.3%; Score 224.2; DB 1; Length 581;
Best Local Similarity 88.5%; Pred. No. 4.4e-65;
Matches 276; Conservative 1; Mismatches 30; Indels 5; Gaps 3;

QY 1 AAATGCGATAAGTAATGTAATTCAGAAATTCAGTAATCATCGAAATCTTTGAACGCACA 60
Db 253 AAATGCGATAAGTAATGTAATTCAGAAATTCAGTAATCATCGAAATCTTTGAACGCACA 312
QY 61 TTGGCGCCCGCCAGATATCTGGCGGCGCATGCGCTGTTGAGCGGTCAATTTCAACCCCTCAAGCC 120
Db 313 TTGGCGCCCGCCAGATATCTGGCGGCGCATGCGCTGTTGAGCGGTCAATTTCAACCCCTCAAGCC 372
QY 121 CCCGGGTTTGGTGTGGGATCGGCAAG-CCCTTGGCGGCAAGCCGCGCCCGCAAAATCTAGT 179
Db 373 CCCGGGTTTGGTGTGGGATCGGCAAG-CCCTTGGCGGCAAGCCGCGCCCGCAAAATCTAGT 432
QY 180 GGCGGTCTCGCTGAGCTTCCATTCGCTAGTAGTAAGAAACCTCGCAACTGGTACGCGCGC 239
Db 433 GGCGGTCTCGCTGAGCTTCCATTCGCTAGTAGTAAGAAACCTCGCAACTGGTACGCGCGC 489
QY 240 CGGCAAGCCGTTAAACCCCAACTTCTG-AAATGTTGACCTCGGATCAGGTAGGAATACC 298
Db 490 TGCCACAGCGGTTAAACCCCAACTTCTGAAAGGTTGACCTCGGATCAGGTAGGAATACC 549
QY 299 CGCTGAACCTTAA 310
Db 550 CGCTGAACCTTAA 561

RESULT 8
US-08-652-127C-5
; Sequence 5, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; ADDRESSEE: Seaby & MacLean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24, 034
; REFERENCE/DOCKET NUMBER: 1898
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 594
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-652-127C-5
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; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC Compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Fusarium poae
; INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
; INDIVIDUAL ISOLATE: sequence)
; IMMEDIATE SOURCE:
; CLONE: pCRFpoaeT427(1-2), pCRFpoaeT534(2-2), and
; CLONE: pCRFpoaeT756(3-1)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /note= "3' end of small subunit
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..180
; OTHER INFORMATION: /note= "ITS 1"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 181..337
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 338..489
; OTHER INFORMATION: /note= "ITS 2"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 490..546
; OTHER INFORMATION: /note= "5' end of large subunit
; OTHER INFORMATION: rRNA gene"
;
; US-08-905-314A-22
;
; Query Match 60.5%; Score 187.6; DB 1; Length 546;
; Best Local Similarity 84.5%; Pred. No. 8.1e-53;
; Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4
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; Qy 1 AAATGCGATAGTAATGTGAATTCGAAATTCGAAATTCAGTGAATCATCGAATCTTTTGAACGCACA 60
; Db 231 AAATGCGATAGTAATGTGAATTCGAAATTCAGTGAATTCAGTGAATTCGAAATCTTTTGAACGCACA 290
;
; Qy 61 TTGGCCCGCCGACGATATTCCTGGCGGGCATGCCCTGTTTCGAGCGTCATTTCAACCCCTCAAGCC 120
; Db 291 TTGGCCCGCCGACGATATTCGCGGGGCATGCCCTGTTTCGAGCGTCATTTCAACCCCTCAAGCC 350
;
; Qy 121 CCCGGGTTTGTTGTTGGGGATCGGCAAGCCCTTTCGGCGCAAGCCGCGCCCGCGAAATCTAGTG 180
; Db 351 C---AGCTTGGTGTGGG-----ATCTGTGTGCAAAACACAGTCCCCCAATGTGATTG 398
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; Qy 181 GCGGCTCTCGTGCAGCTTCCATTCGCTAGTAGTAAACCCCTCGCAACTGTTGTAACGCGCGC 240

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; OTHER INFORMATION: /note= "ITS 2"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 473..504
; OTHER INFORMATION: /note= "5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
US-08-887-480-82

Query Match      60.2%; Score 186.6; DB 1; Length 504;
Best Local Similarity 82.6%; Pred. No. 1.7e-52;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;

QY 1 AAATGCGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
Db 212 AAATGCGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 271

QY 61 TTGCGCGCCGCGATTTCTGGCGGCATGCTGTCGAGCGTCATTTCAACCTCAAGCC 120
Db 272 TTGCGCGCCGCGATTTCTGGCGGCATGCTGTCGAGCGTCATTTCAACCTCAAGCC 331

QY 121 CCCGGGTTTGGTGTGGGATCGGCAAGCCCTTTGCGGCAAGCGCGCCGAAATCTAGTG 180
Db 332 C---AGCTTGGTGTGGG-----AGCTGCAGTCTGCTGCACCTCCCAATACATTG 380

QY 181 GCGGTCTGCTGCGAGCTTCCATTTGCGGTAGTAGTAAACCTTCGCAACTGCTAGCGGCGC 240
Db 381 GCGGTCAAGTCGAGCTTCCATAGCGTAGTAATTTACATATCGTTACTGTTAATCGTCGC 440

QY 241 GCGCAAGCGGTAAACCCCACTCTGAAATGTTGACCTCGGATCAGTAGGAATACCGC 300
Db 441 GCGYACGCGGTAAA-CCCCAACTTCTGAATGTTGACCTCGGATCAGTAGGAATACCGC 499

QY 301 CTGAA 305
Db 500 CTGAA 504
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RESULT 12

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US-08-905-314A-19
; Sequence 19, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827695artis Corporation Patent Department
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 base pairs
; TYPE: nucleic acid
```

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Fusarium culmorum
; INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
; INDIVIDUAL ISOLATE: (consensus sequence)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..12
; OTHER INFORMATION: /note= "3' end of small subunit"
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 13..161
; OTHER INFORMATION: /note= "ITS 1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 162..318
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 319..472
; OTHER INFORMATION: /note= "ITS 2"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 473..504
; OTHER INFORMATION: /note= "5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
US-08-905-314A-19

Query Match      60.2%; Score 186.6; DB 1; Length 504;
Best Local Similarity 82.6%; Pred. No. 1.7e-52;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;

QY 1 AAATGCGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
Db 212 AAATGCGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 271

QY 61 TTGCGCGCCGCGATTTCTGGCGGCATGCTGTCGAGCGTCATTTCAACCTCAAGCC 120
Db 272 TTGCGCGCCGCGATTTCTGGCGGCATGCTGTCGAGCGTCATTTCAACCTCAAGCC 331

QY 121 CCCGGGTTTGGTGTGGGATCGGCAAGCCCTTTGCGGCAAGCGCGCCGAAATCTAGTG 180
Db 332 C---AGCTTGGTGTGGG-----AGCTGCAGTCTGCTGCACCTCCCAATACATTG 380

QY 181 GCGGTCTGCTGCGAGCTTCCATTTGCGGTAGTAGTAAACCTTCGCAACTGCTAGCGGCGC 240
Db 381 GCGGTCAAGTCGAGCTTCCATAGCGTAGTAATTTACATATCGTTACTGTTAATCGTCGC 440

QY 241 GCGCAAGCGGTAAACCCCACTTCTGAATGTTGACCTCGGATCAGTAGGAATACCGC 300
Db 441 GCGYACGCGGTAAA-CCCCAACTTCTGAATGTTGACCTCGGATCAGTAGGAATACCGC 499

QY 301 CTGAA 305
Db 500 CTGAA 504
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RESULT 13

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US-08-722-187-82
; Sequence 82, Application US/08722187
; Patent No. 5955274
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
```

APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
US-08-722-187-82

Query Match 60.2%; Score 186.6; DB 2; Length 504;
Best Local Similarity 82.6%; Pred. No. 1.7e-52;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;
Qy 1 AAATGCGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
Db 212 AAATGCGATAAGTAATGTGAATTCGAGATTCAGTGAATCATCGAATCTTTGAACGCACA 271
Qy 61 TTGCGCCCGCAGTATTTCTGGCGGCATGCGTCTTTCGAGCGTCAATTTCAACCCCTCAAGCC 120
Db 272 TTGCGCCCGCAGTATTTCTGGCGGCATGCGTCTTTCGAGCGTCAATTTCAACCCCTCAAGCC 331
Qy 121 CCCGGGTTTGGTCTTGGGATCGGCAAGCCCTTTCGCGCAAGCCGCGCCCGAAATCTAGTG 180
Db 332 C---AGCTTGGTGTGGG-----AGCTGCAGTCTCTGTCGACTCCCCAAATACATTG 380
Qy 181 GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAACCCCTCGCAACTGGTAGCGCGCGC 240
Db 381 GCGGTACGTCGRAGCTTCATAGCGTAGTAAATTACATATCGTACTGTAATCGTCGC 440
Qy 241 GGCCAAAGCGGTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 300
Db 441 GGCYACGCGGTAAA-CCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 499
Qy 301 CTGAA 305
Db 500 CTGAA 504

RESULT 14

PCT-US95-04712-82

; Sequence 82, Application PC/TUS9504712
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M

APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
PCT-US95-04712-82

Query Match 60.2%; Score 186.6; DB 5; Length 504;
Best Local Similarity 82.8%; Pred. No. 1.7e-52;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;
Qy 1 AAATGCGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
Db 212 AAATGCGATAAGTAATGTGAATTCGAGATTCAGTGAATCATCGAATCTTTGAACGCACA 271
Qy 61 TTGCGCCCGCAGTATTTCTGGCGGCATGCGTCTTTCGAGCGTCAATTTCAACCCCTCAAGCC 120
Db 272 TTGCGCCCGCAGTATTTCTGGCGGCATGCGTCTTTCGAGCGTCAATTTCAACCCCTCAAGCC 331
Qy 121 CCCGGGTTTGGTCTTGGGATCGGCAAGCCCTTTCGCGCAAGCCGCGCCCGAAATCTAGTG 180
Db 332 C---AGCTTGGTGTGGG-----AGCTGCAGTCTCTGTCGACTCCCCAAATACATTG 380
Qy 181 GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAACCCCTCGCAACTGGTAGCGCGCGC 240
Db 381 GCGGTACGTCGRAGCTTCATAGCGTAGTAAATTACATATCGTACTGTAATCGTCGC 440
Qy 241 GGCCAAAGCGGTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 300
Db 441 GGCYACGCGGTAAA-CCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 499
Qy 301 CTGAA 305
Db 500 CTGAA 504

Search completed: October 23, 2005, 16:07:06
Job time : 185.825 secs

RESULT 15
US-08-986-727-4
; Sequence 4, Application US/08986727
; Patent No. 6080543
; GENERAL INFORMATION:
; APPLICANT: ENGEL, Stacia R.
; APPLICANT: DESCENZO, Richard A.
; APPLICANT: IRELAN, Nancy A.
; TITLE OF INVENTION: DETECTION OF FUNGAL PATHOGENS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,727
; FILING DATE: 08-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ekstrom, Richard C.
; REGISTRATION NUMBER: 37,027
; REFERENCE/DOCKET NUMBER: 009773-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 611 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-986-727-4

Query Match 59.7%; Score 185; DB 3; Length 611;
Best Local Similarity 83.1%; Pred. No. 6.3e-52;
Matches 260; Conservative 0; Mismatches 45; Indels 8; Gaps 4;

QY 1 AAATCGGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
Db |||||
283 AAATCGGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 342

QY 61 TTGCGCCGCCAGTATTCTGGCGGGGATGCTTTCGAGCGTCATTCAACCTCAAGCC 120
Db |||||
343 TTGCGCCCTCTGCTATTCCGAGGGGATGCTTTCGAGCGTCATTCAACCTCAAG-- 400

QY 121 CCCGGGTTGGTGTGGGGATCGCAAGCCCTTGGCGAAGCGCGCCCGCAAAATCTAGTG 180
Db |||||
401 -CCTGGCTGGTGTGGGGCACTGTCCCGCCCGGGGAGCAGGCCCTGAATCCAGTG 459

QY 181 GCGGTCCTGCTCAGCTTCATTTGGGTAGTAAACCCCTCGCAACTG--GTACGCGGC 238
Db |||||
460 GCGAGCTGCG--CAGGACCCGAGCGCAGTAGTTAAACCTCGCTCCGGAGGCCCTGCG 517

QY 239 GCGGCCAGCCCTTAACCCCACTTCTGAATG-TTGACCTCGGATCAGGTAGGAATAC 297
Db |||||
518 GTGCGCCTGCCCTTAACCCCACTTCTGAAGTTTGACCTCGGATCAGGTAGGAATAC 577

QY 298 CCGCTGAACCTTAA 310
Db |||||
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
1907.926 Million cell updates/sec

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Perfect score: 310
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Gapop 10.0 , Gapext 1.0

Searched: 9772231 segs, 4124568258 residues
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Maximum DB seq length: 2000000000

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Maximum Match 100%
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19:	/cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20:	/cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21:	/cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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24:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
25:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	310	100.0	310	15	US-10-046-955-7
2	302.8	97.7	534	10	US-09-961-755A-7
3	302.8	97.7	534	20	US-10-773-904-7
4	302.8	97.7	534	20	US-10-773-905-7
5	240.2	77.5	319	15	US-10-046-955-6
6	233.4	75.3	552	21	US-10-829-661-5
7	233.4	75.3	552	21	US-10-672-300-5

8	194.4	62.7	522	10	US-09-961-755A-5
9	194.4	62.7	522	10	US-09-961-755A-8
10	194.4	62.7	522	10	US-10-773-904-5
11	194.4	62.7	522	20	US-10-773-904-8
12	194.4	62.7	522	20	US-10-773-905-5
13	194.4	62.7	522	20	US-10-773-905-8
c 14	181	58.4	780	20	US-10-425-115-137730
15	179.2	57.8	521	10	US-09-961-755A-6
16	179.2	57.8	521	20	US-10-773-904-6
17	179.2	57.8	521	20	US-10-773-905-6
18	138	44.5	596	21	US-10-829-661-1
19	138	44.5	596	21	US-10-672-300-1
20	136.2	43.9	652	16	US-10-121-740-2
21	136.2	43.9	652	19	US-10-623-432-2
22	136.2	43.9	652	24	US-11-131-659-2
23	136	43.9	365	15	US-10-046-955-3
24	135.4	43.7	528	22	US-10-757-093-29
25	131.4	42.4	364	15	US-10-046-955-2
26	125	40.3	309	15	US-10-046-955-28
27	124.6	40.2	641	9	US-09-766-173C-4
28	124.2	40.1	650	16	US-10-121-740-4
29	124.2	40.1	650	19	US-10-623-432-4
30	124.2	40.1	650	24	US-11-131-659-4
31	123.2	39.7	365	15	US-10-046-955-5
32	121.4	39.2	577	22	US-10-757-093-28
33	120.2	38.8	618	9	US-09-766-173C-5
34	111.6	36.0	343	15	US-10-046-955-27
35	111.6	36.0	344	15	US-10-046-955-26
36	110.4	35.6	377	9	US-09-961-663-14
37	110.4	35.6	377	9	US-09-961-663-15
38	110.4	35.6	377	9	US-09-961-663-16
39	110.4	35.6	377	9	US-09-961-663-19
40	110	35.5	466	17	US-10-356-320-1
41	108.8	35.1	336	15	US-10-046-955-29
42	108.4	35.0	534	9	US-09-961-663-17
43	107.8	34.8	346	15	US-10-046-955-25
44	107.2	34.6	346	15	US-10-046-955-24
45	107.2	34.6	540	9	US-09-961-663-18

ALIGNMENTS

RESULT 1

US-10-046-955-7
; Sequence 7, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Di
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Liliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; TITLE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-10-046-955-7

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Query Match      100.0%; Score 310; DB 15; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-102;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATGCGGATAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
Db 1 AAATGCGGATAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60

Qy 61 TTGCGCCCGCCAGATTTCTGCGGGGCATGCTGTTGAGCGGTCAATTTCAACCCCTCAAGCC 120
Db 61 TTGCGCCCGCCAGATTTCTGCGGGGCATGCTGTTGAGCGGTCAATTTCAACCCCTCAAGCC 120

Qy 121 CCCGGGTTTGGTGTGGGATCGCAAGCCCTTCGCGCAAGCCGCGCCGCGAAATCTAGTG 180
Db 121 CCCGGGTTTGGTGTGGGATCGCAAGCCCTTCGCGCAAGCCGCGCCGCGAAATCTAGTG 180

Qy 181 GCGGTCTCGCTGCAGCTTCCATTCGGTAGTAGTAAACCCCTCGCAACTGGTACGCGGCG 240
Db 181 GCGGTCTCGCTGCAGCTTCCATTCGGTAGTAGTAAACCCCTCGCAACTGGTACGCGGCG 240

Qy 241 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 300
Db 241 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 300

Qy 301 CTGAAC TAA 310
Db 301 CTGAAC TAA 310

RESULT 2
US-09-961-755A-7
; Sequence 7, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7

Query Match      97.7%; Score 302.8; DB 10; Length 534;
Best Local Similarity 99.3%; Pred. No. 1.1e-99;
Matches 304; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAATGCGGATAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
Db 229 AAATGCGGATAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 288

Qy 61 TTGCGCCCGCCAGATTTCTGCGGGGCATGCTGTTGAGCGGTCAATTTCAACCCCTCAAGCC 120
Db 289 TTGCGCCCGCCAGATTTCTGCGGGGCATGCTGTTGAGCGGTCAATTTCAACCCCTCAAGCC 348

Qy 121 CCCGGGTTTGGTGTGGGATCGCAAGCCCTTCGCGCAAGCCGCGCCGCGAAATCTAGTG 180
Db 349 CCCGGGTTTGGTGTGGGATCGCAAGCCCTTCGCGCAAGCCGCGCCGCGAAATCTAGTG 408

Qy 181 GCGGTCTCGCTGCAGCTTCCATTCGGTAGTAGTAAACCCCTCGCAACTGGTACGCGGCG 240
Db 409 GCGGTCTCGCTGCAGCTTCCATTCGGTAGTAGTAAACCCCTCGCAACTGGTACGCGGCG 468

Qy 241 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 300
Db 469 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 528

Qy 301 CTGAAC TAA 310
Db 301 CTGAAC TAA 310

Query Match      97.7%; Score 302.8; DB 10; Length 534;
Best Local Similarity 99.3%; Pred. No. 1.1e-99;
Matches 304; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAATGCGGATAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
Db 229 AAATGCGGATAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 288

Qy 61 TTGCGCCCGCCAGATTTCTGCGGGGCATGCTGTTGAGCGGTCAATTTCAACCCCTCAAGCC 120
Db 289 TTGCGCCCGCCAGATTTCTGCGGGGCATGCTGTTGAGCGGTCAATTTCAACCCCTCAAGCC 348

Qy 121 CCCGGGTTTGGTGTGGGATCGCAAGCCCTTCGCGCAAGCCGCGCCGCGAAATCTAGTG 180
Db 349 CCCGGGTTTGGTGTGGGATCGCAAGCCCTTCGCGCAAGCCGCGCCGCGAAATCTAGTG 408

Qy 181 GCGGTCTCGCTGCAGCTTCCATTCGGTAGTAGTAAACCCCTCGCAACTGGTACGCGGCG 240
Db 409 GCGGTCTCGCTGCAGCTTCCATTCGGTAGTAGTAAACCCCTCGCAACTGGTACGCGGCG 468

Qy 241 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 300
Db 469 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 528
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Qy 301 CTGAAC 306
Db 529 CTGAAC 534

RESULT 3
US-10-773-904-7
; Sequence 7, Application US/10773904
; Publication No. US20040259120A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/10/773,904
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/09/961,755
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-10-773-904-7

Query Match      97.7%; Score 302.8; DB 20; Length 534;
Best Local Similarity 99.3%; Pred. No. 1.1e-99;
Matches 304; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAATGCGGATAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
Db 229 AAATGCGGATAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 288

Qy 61 TTGCGCCCGCCAGATTTCTGCGGGGCATGCTGTTGAGCGGTCAATTTCAACCCCTCAAGCC 120
Db 289 TTGCGCCCGCCAGATTTCTGCGGGGCATGCTGTTGAGCGGTCAATTTCAACCCCTCAAGCC 348

Qy 121 CCCGGGTTTGGTGTGGGATCGCAAGCCCTTCGCGCAAGCCGCGCCGCGAAATCTAGTG 180
Db 349 CCCGGGTTTGGTGTGGGATCGCAAGCCCTTCGCGCAAGCCGCGCCGCGAAATCTAGTG 408

Qy 181 GCGGTCTCGCTGCAGCTTCCATTCGGTAGTAGTAAACCCCTCGCAACTGGTACGCGGCG 240
Db 409 GCGGTCTCGCTGCAGCTTCCATTCGGTAGTAGTAAACCCCTCGCAACTGGTACGCGGCG 468

Qy 241 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 300
Db 469 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 528

Qy 301 CTGAAC 306
Db 529 CTGAAC 534

RESULT 4
US-10-773-905-7
; Sequence 7, Application US/10773905
; Publication No. US20040259121A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/10/773,905
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/09/961,755
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-10-773-905-7

Query Match      97.7%; Score 302.8; DB 20; Length 534;
Best Local Similarity 99.3%; Pred. No. 1.1e-99;
Matches 304; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGCGCATAGTAATGTAATTCGAAATTCAGTGAATCATCGAAATCTTTGAACGCACA 60
DB 229 AATGCGCATAGTAATGTAATTCGAAATTCAGTGAATCATCGAAATCTTTGAACGCACA 288

QY 61 TTGCGCCGCCAGTATTCTGCGGGCATGCTGTTCGAGCGTCATTTCAACCCCTCAAGCC 120
DB 289 TTGCGCCGCCAGTATTCTGCGGGCATGCTGTTCGAGCGTCATTTCAACCCCTCAAGCC 348

QY 121 CCCGGGTTTGGTGTTCGGGATCGGCAAGCCCTTCGCGCAAGCCGGCCCCGAAATCTAGTG 180
DB 349 CCCGGGTTTGGTGTTCGGGATCGGCGAGCCCTTCGCGCAAGCCGGCCCCGAAATCTAGTG 408

QY 181 GCGGTCCTGCTCGAGCTTCCATTTCGCTAGTAGTAAAAACCCCTCGCAACTGGTAGCGCGCGC 240
DB 409 GCGGTCCTGCTCGAGCTTCCATTTCGCTAGTAGTAAAAACCCCTCGCAACTGGTAGCGCGCGC 468

QY 241 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGTAGGAATACCCG 300
DB 469 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGTAGGAATACCCG 528

QY 301 CTGAAC 306
DB 529 CTGAAC 534

RESULT 5
US-10-046-955-6
; Sequence 6, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Lilliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; TITLE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
US-10-046-955-6

Query Match      77.5%; Score 240.2; DB 15; Length 319;
Best Local Similarity 87.4%; Pred. No. 7.2e-77;
Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;

QY 1 AATGCGCATAGTAATGTAATTCGAAATTCAGTGAATCATCGAAATCTTTGAACGCACA 60
DB 3 AATGCGCATAGTAATGTAATTCGAAATTCAGTGAATCATCGAAATCTTTGAACGCACA 62

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Qy	61	TTGGCCCGCCAGATATTCTCGCGGGCATGCTGTTCAGAGCGTCAATTTCAACCCCTCAAGCC	120
Db	63	TTGGCCCGCCAGATATTCTCGCGGGCATGCTGTTCAGAGCGTCAATTTCAACCCCTCAGGCC	122
Qy	121	CCCGGGTTTCGTGTGGGGATCGCAAGCCCTTTCGGC-----AAGCCGGCCCGGAAA	173
Db	123	CCCGGGCTTGGGTGTGGGGATCGCGGAAGCCCTCTCGGGGCACAAGCCCGTCCCCCAAA	182
Qy	174	TCTAGTGGCGGTCTCGCTGCAGCTTCCATTTGCGTAGTAGTAAAAACCCCTCGCAACTGGTAC	233
Db	183	TACAGTGGCGGTCCCGCGCAGCTTCCATTTGCGTAGTAGTAAACACCTCGCAACTGGAGA	242
Qy	234	GCGGCGGGCCAGACCGTTTAAACCCCAACTTCTGAATGTTGACTTCGGATCAGGTAGGA	293
Db	243	GCGGCGGGCCAGCCCGTAAAAACCCCAACTTCTGAATGTTGACTTCGAATCAGGTAGGA	302
Qy	294	ATACCCGCTGAACCTTAA	310
Db	303	ATACCCGCTGAACCTTAA	319
RESULT 6			
US-10-829-661-5			
; Sequence 5, Application US/10829661			
; Publication No. US20050009051A1			
; GENERAL INFORMATION:			
; APPLICANT: HAN, XIANG-YANG			
; APPLICANT: TARRAND, JEFFREY J.			
; APPLICANT: PHAM, AUDREY S.			
; APPLICANT: MAY, GREGORY S.			
; TITLE OF INVENTION: DIAGNOSIS OF MOULD INFECTION			
; FILE REFERENCE: UTSC865US			
; CURRENT APPLICATION NUMBER: US/10/829,661			
; CURRENT FILING DATE: 2004-04-21			
; PRIOR APPLICATION NUMBER: 10/672,300			
; PRIOR FILING DATE: 2003-09-26			
; PRIOR APPLICATION NUMBER: 60/414,008			
; PRIOR FILING DATE: 2002-09-27			
; NUMBER OF SEQ ID NOS: 29			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 5			
; LENGTH: 552			
; TYPE: DNA			
; ORGANISM: Fusarium sp.			
US-10-829-661-5			
Query Match 75.3%; Score 233.4; DB 21; Length 552;			
Best Local Similarity 88.0%; Pred. No. 2.8e-74;			
Matches 279; Conservative 0; Mismatches 31; Indels 7; Gaps 2;			
Qy	1	AAATGCGATAAGTAATCTGAATTTGCAAAATTCAGTGAATCATCGAATCTTTTGAACGCACA	60
Db	236	AAACGCGATAGTAATGTAATTTGCAAAATTCAGTGAATCATCGAATCTTTTGAACGCACA	295
Qy	61	TTGGCCCGCCAGATATTCTCGCGGGCATGCTGTTCAGAGCGTCAATTTCAACCCCTCAAGCC	120
Db	296	TTGGCCCGCCAGATATTCTCGCGGGCATGCTGTTCAGAGCGTCAATTTCAACCCCTCAGGCC	355
Qy	121	CCCGGGTTTCGTGTGGGGATCGGCAAG-----CCCTTGGGGAAGCGGGCCCCGAAATC	175
Db	356	CCCGGGCTTCGTGTGGGGATCGGTTCGGAGCCCTTCGGGGGCACACGCCGTCGCCCAATT	415
Qy	176	TAGTGGGGTTCGCTGCAGCTTCCATTGCGTAGTGTAAACCCCTCGCAACTCGTAGCG	235
Db	416	CAGTGGGGTTCGCTGCAGCTTCCATTGCGTAGTGTAAACCCCTCGCAACTCGTAGCG	475
Qy	236	GGCGGGCCCAAGCCGTTAAAA--CCCCCAACTTCTGAATGTTGACTTCGGATCAGGTAGGA	293
Db	476	GGCGGGCCCAAGCCGTTAAAAACCCCAACTTCTGAATGTTGACTTCGGATCAGGTAGGA	535
Qy	294	ATACCCGCTGAACCTTAA	310

Qy	61	TTGGCCCGCCAGATATTCTCGCGGGCATGCTGTTCAGAGCGTCAATTTCAACCCCTCAAGCC	120
Db	63	TTGGCCCGCCAGATATTCTCGCGGGCATGCTGTTCAGAGCGTCAATTTCAACCCCTCAGGCC	122
Qy	121	CCCGGGTTTCGTGTGGGGATCGCAAGCCCTTTCGGC-----AAGCCGGCCCGGAAA	173
Db	123	CCCGGGCTTGGGTGTGGGGATCGCGGAAGCCCTCTCGGGGCACAAGCCCGTCCCCCAAA	182
Qy	174	TCTAGTGGCGGTCTCGCTGCAGCTTCCATTTGCGTAGTAGTAAAAACCCCTCGCAACTGGTAC	233
Db	183	TACAGTGGCGGTCCCGCGCAGCTTCCATTTGCGTAGTAGTAAACACCTCGCAACTGGAGA	242
Qy	234	GCGGCGGGCCAGCGCTTTAAACCCCAACTTCTGAATGTTGACTTCGGATCAGGTAGGA	293
Db	243	GCGGCGGGCCAGCGCTTAAACACCCCAACTTCTGAATGTTGACTTCGAATCAGGTAGGA	302
Qy	294	ATACCCGCTGAACCTTAA	310
Db	303	ATACCCGCTGAACCTTAA	319
RESULT 6			
US-10-829-661-5			
; Sequence 5, Application US/10829661			
; Publication No. US20050009051A1			
; GENERAL INFORMATION:			
; APPLICANT: HAN, XIANG-YANG			
; APPLICANT: TARRAND, JEFFREY J.			
; APPLICANT: PHAM, AUDREY S.			
; APPLICANT: MAY, GREGORY S.			
; TITLE OF INVENTION: DIAGNOSIS OF MOULD INFECTION			
; FILE REFERENCE: UTSC865US			
; CURRENT APPLICATION NUMBER: US/10/829,661			
; CURRENT FILING DATE: 2004-04-21			
; PRIOR APPLICATION NUMBER: 10/672,300			
; PRIOR FILING DATE: 2003-09-26			
; PRIOR APPLICATION NUMBER: 60/414,008			
; PRIOR FILING DATE: 2002-09-27			
; NUMBER OF SEQ ID NOS: 29			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 5			
; LENGTH: 552			
; TYPE: DNA			
; ORGANISM: Fusarium sp.			
US-10-829-661-5			
Query Match 75.3%; Score 233.4; DB 21; Length 552;			
Best Local Similarity 88.0%; Pred. No. 2.8e-74;			
Matches 279; Conservative 0; Mismatches 31; Indels 7; Gaps 2;			
Qy	1	AAATGCGATAAGTAATCTGAATTTGCAAAATTCAGTGAATCATCGAATCTTTTGAACGCACA	60
Db	236	AAACGCGATAGTAATGTAATTTGCAAAATTCAGTGAATCATCGAATCTTTTGAACGCACA	295
Qy	61	TTGGCCCGCCAGTATTCTCGCGGGCATGCTGTTCAGAGCGTCAATTTCAACCCCTCAAGCC	120
Db	296	TTGGCCCGCCAGTATTCTCGCGGGCATGCTGTTCAGAGCGTCAATTTCAACCCCTCAGGCC	355
Qy	121	CCCGGGTTTCGTGTGGGGATCGGCAAG-----CCCTTGGGGGAGCGGGCCCCGAAATC	175
Db	356	CCCGGGCTTCGTGTGGGGATCGGTTCGGAGCCCTTCGGGGGACACGCGCGTCCCCCAATT	415
Qy	176	TAGTGGGGTTCGCTGCAGCTTCCATTGCGTAGTGTAAACCCCTCGCAACTCGTAGCG	235
Db	416	CAGTGGGGTTCGCTGCAGCTTCCATTGCGTAGTGTAAACCCCTCGCAACTCGTAGCG	475
Qy	236	GGCGCGGCCAAGCGGTTTAAA--CCCCCAACTTCTGAATGTTGACTTCGGATCAGGTAGGA	293
Db	476	GGCGCGGCCAAGCGGTTTAAAACCCCCCAACTTCTGAATGTTGACTTCGGATCAGGTAGGA	535
Qy	294	ATACCCGCTGAACCTTAA	310

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Db 536 ATACCCGCTGAACCTTAA 552
; Query Match 75.3%; Score 233.4; DB 21; Length 552;
; Best Local Similarity 88.0%; Pred. No. 2.8e-74;
; Matches 279; Conservative 0; Mismatches 31; Indels 7; Gaps 2;

RESULT 7
US-10-672-300-5
; Sequence 5, Application US/10672300
; Publication No. US20050048509A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: TARRAND, JEFFREY J.
; TITLE OF INVENTION: DIAGNOSIS OF INVASIVE MOLD INFECTION
; FILE REFERENCE: UTXC:766US
; CURRENT APPLICATION NUMBER: US/10/672,300
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/414,008
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Fusarium sp.
US-10-672-300-5

Query Match 75.3%; Score 233.4; DB 21; Length 552;
Best Local Similarity 88.0%; Pred. No. 2.8e-74;
Matches 279; Conservative 0; Mismatches 31; Indels 7; Gaps 2;

Qy 1 AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAAATCTTTTGAACGCACA 60
Db 236 AAACGCGATAAGTAATGTGAATTGCGAATTTAGTGAATCATCGAAATCTTTTGAACGCACA 295
Qy 61 TTGGCGCGCCGAGTATTCCTGCGGGGATGCGCTGTCAGGCGTCAATTTCAACCCCTCAAGCC 120
Db 296 TTGGCGCGCCGAGTATTCCTGCGGGGATGCGCTGTCAGGCGTCAATTTCAACCCCTCAAGCC 355
Qy 121 CCCGGGTTTGGTGTGGGGATCGGCAAG----CCCTTGGCGCAAGCGCGCCCGGAATC 175
Db 356 CCCGGGCTGGTGTGGGGATCGTTCGAGCCCTCCGGGGCACAGCGCTCCGCCAATTT 415
Qy 176 TAGTGGCGGCTCTCGCTGCAGCTTCCATTTGGGTAGTAGTAAACCCCTCGCAACTGGTACGC 235
Db 416 CAGTGGCGGCTCTCGCTGCAGCTTCCATTTGGGTAGTAGTAAACCCCTCGCAACTGGAAGGC 475
Qy 236 GGCGCGGCAAGCCGTTAAA--CCCCAACTTCTGAATGTTGACCTCGATCAGGTAGGA 293
Db 476 GGCGCGGCAAGCCGTTAAAACCCCCCAACTTCTGAATGTTGACCTCGATCAGGTAGGA 535
Qy 294 ATACCCGCTGAACCTTAA 310
Db 536 ATACCCGCTGAACCTTAA 552

RESULT 8
US-09-961-755A-5
; Sequence 5, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 5
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium subglutinans
US-09-961-755A-5

Query Match 62.7%; Score 194.4; DB 10; Length 522;
Best Local Similarity 84.3%; Pred. No. 5.1e-60;
Matches 258; Conservative 0; Mismatches 36; Indels 12; Gaps 3;

Qy 1 AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAAATCTTTTGAACGCACA 60
Db 229 AAATGCGATAAGTAATGTGAATTGCGAATTCAGTGAATCATCGAAATCTTTTGAACGCACA 288
Qy 61 TTGGCGCGCCGAGTATTCCTGCGGGGATGCGCTGTCAGGCGTCAATTTCAACCCCTCAAGCC 120
Db 289 TTGGCGCGCCGAGTATTCCTGCGGGGATGCGCTGTCAGGCGTCAATTTCAACCCCTCAAGCC 348
Qy 121 CCCGGGTTTGGTGTGGGGATCGGCAAGCCCTTTCGCGCAAGCGCGCCCGAAATCTAGTG 180
Db 349 C-----AGCTTGGTGTTCGGACTTCGCGAGTCAAAATCGCGTTCCTCCCAAAATTTGATTG 398
Qy 181 GCGGTCTCGCTGCAGCTTCCATTTGCGGTAGTAGTAAACCCCTCGCAACTGGTAGCGCGCGC 240
Db 399 GCGGTCAAG--TCGAGCTTCCATAGCGTAGTAGTAAACCCCTCGTACTGTTAATCGTGGC 457
Qy 241 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 300
Db 458 GGCCAAAGCCGTTAAAC--CCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 516

RESULT 9
US-09-961-755A-8
; Sequence 8, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 8
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
US-09-961-755A-8

Query Match 62.7%; Score 194.4; DB 10; Length 522;
Best Local Similarity 84.3%; Pred. No. 5.1e-60;
Matches 258; Conservative 0; Mismatches 36; Indels 12; Gaps 3;

Qy 1 AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAAATCTTTTGAACGCACA 60
Db 229 AAATGCGATAAGTAATGTGAATTGCGAATTCAGTGAATCATCGAAATCTTTTGAACGCACA 288
Qy 61 TTGGCGCGCCGAGTATTCCTGCGGGGATGCGCTGTCAGGCGTCAATTTCAACCCCTCAAGCC 120
Db 289 TTGGCGCGCCGAGTATTCCTGCGGGGATGCGCTGTCAGGCGTCAATTTCAACCCCTCAAGCC 348
Qy 121 CCCGGGTTTGGTGTGGGGATCGGCAAGCCCTTTCGCGCAAGCGCGCCCGAAATCTAGTG 180
Db 349 C-----AGCTTGGTGTTCGGACTTCGCGAGTCAAAATCGCGTTCCTCCCAAAATTTGATTG 398
Qy 181 GCGGTCTCGCTGCAGCTTCCATTTGCGGTAGTAGTAAACCCCTCGCAACTGGTAGCGCGCGC 240
Db 399 GCGGTCAAG--TCGAGCTTCCATAGCGTAGTAGTAAACCCCTCGTACTGTTAATCGTGGC 457
Qy 241 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 300
Db 458 GGCCAAAGCCGTTAAAC--CCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 516
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QY 301 CTGAAC 306
Db 517 CTGAAC 522

RESULT 10
US-10-773-904-5
; Sequence 5, Application US/10773904
; Publication No. US20040259120A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/10/773,904
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/09/961,755
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium subglutinans
US-10-773-904-5

Query Match 62.7%; Score 194.4; DB 20; Length 522;
Best Local Similarity 84.3%; Pred. No. 5.1e-60;
Matches 258; Conservative 0; Mismatches 36; Indels 12; Gaps 3;

QY 1 AAATCGGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
Db 229 AAATCGGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 288

QY 61 TTGCGCCCGCCAGTATCTCGCGGCATCCCTGTTGAGCGGTCATTTCAACCCCTCAAGCC 120
Db 289 TTGCGCCCGCCAGTATCTCGCGGCATCCCTGTTGAGCGGTCATTTCAACCCCTCAAGCC 348

QY 121 CCGGGTTTGGTGTGGGATCGGCAAGCCCTTGGCGGAGCGGCCGCCGGAATCTAGTG 180
Db 349 C-----AGCTTGGTGTGGGACTCGCGAGTCAAAATCCGTTCCCAAAATGATTG 398

QY 181 GGGTCTCGTCGACGTTCCATTGCGTAGTAGTAAACCCCTCGCAACTGGTACGGCGGC 240
Db 399 GCGGTACAG-TGAGCTTCCATTGCGTAGTAGTAAACCCCTCGTACTGTTAATCGTCC 457

QY 241 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 300
Db 458 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 516

QY 301 CTGAAC 306
Db 517 CTGAAC 522

RESULT 12
US-10-773-905-5
; Sequence 5, Application US/10773905
; Publication No. US20040259121A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/10/773,905
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/09/961,755
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium subglutinans
US-10-773-905-5

Query Match 62.7%; Score 194.4; DB 20; Length 522;
Best Local Similarity 84.3%; Pred. No. 5.1e-60;
Matches 258; Conservative 0; Mismatches 36; Indels 12; Gaps 3;

QY 1 AAATCGGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
Db 229 AAATCGGATAAGTAATGTGAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 288

QY 61 TTGCGCCCGCCAGTATCTCGCGGCATCCCTGTTGAGCGGTCATTTCAACCCCTCAAGCC 120
Db 289 TTGCGCCCGCCAGTATCTCGCGGCATCCCTGTTGAGCGGTCATTTCAACCCCTCAAGCC 348

QY 121 CCGGGTTTGGTGTGGGATCGGCAAGCCCTTGGCGGAGCGGCCGCCGGAATCTAGTG 180
Db 349 C-----AGCTTGGTGTGGGACTCGCGAGTCAAAATCCGTTCCCAAAATGATTG 398

QY 181 GGGTCTCGTCGACGTTCCATTGCGTAGTAGTAAACCCCTCGCAACTGGTACGGCGGC 240
Db 399 GCGGTACAG-TGAGCTTCCATTGCGTAGTAGTAAACCCCTCGTACTGTTAATCGTCC 457

QY 241 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 300
Db 458 GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 516

QY 301 CTGAAC 306
Db 517 CTGAAC 522

RESULT 11
US-10-773-904-8
; Sequence 8, Application US/10773904
; Publication No. US20040259120A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/10/773,904
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/09/961,755
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
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Db 399 GCGGTACG-TCGAGCTTCCATAGCGTAGTAGTAAACCCCTCGTACTGTGTAATCGTCGC 457
Qy 241 GGCCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 300
Db 458 GGCCACCGCGTTAAA-CCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 516
Qy 301 CTGAAC 306
Db 517 CTGAAC 522

RESULT 13
US-10-773-905-8
; Sequence 8, Application US/10773905
; Publication No. US2004025912A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/10/773,905
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/09/961,755
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
US-10-773-905-8

Query Match 62.7%; Score 194.4; DB 20; Length 522;
Best Local Similarity 84.3%; Pred. No. 5.1e-60; Indels 12; Gaps 3;
Matches 258; Conservative 0; Mismatches 36;

Qy 1 AAATGCCATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTTGAACGCACA 60
Db 229 AAATGCCATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTTGAACGCACA 288
Qy 61 TTGGCCCGCCGAGTAATCTCGCGGGCATGCTGTTGAGCGTCAATTTCAACCCCTCAAGCC 120
Db 289 TTGGCCCGCCGAGTAATCTCGCGGGCATGCTGTTGAGCGTCAATTTCAACCCCTCAAGCC 348
Qy 121 CCCGGGTTTGGTGTGGGATCGCAAGCCCTTTCGCGCAAGCCCGCCCGAAATCTAGTG 180
Db 349 C-----AGCTTGGTGTGGGACTCGCGAGTCAAAATCGCGTTTCCCAAAATTTGATTG 398
Qy 181 GCGGTCTCGTGCAGCTTCCATTGCGTAGTAGTAAACCCCTCGCAACTGGTAGCGCGCGC 240
Db 399 GCGGTACG-TCGAGCTTCCATAGCGTAGTAGTAAACCCCTCGTACTGTTAATCGTCGC 457
Qy 241 GGCCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 300
Db 458 GGCCACCGCGTTAAA-CCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 516
Qy 301 CTGAAC 306
Db 517 CTGAAC 522

RESULT 14
US-10-425-115-137730/c
; Sequence 137730, Application US/10425115
; Publication No. US2004021427A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
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; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 137730
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(780)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_57087C.1
US-10-425-115-137730

Query Match 58.4%; Score 181; DB 20; Length 780;
Best Local Similarity 79.1%; Pred. No. 4.8e-55;
Matches 242; Conservative 0; Mismatches 56; Indels 8; Gaps 2;

Qy 5 GCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTTGAACGCACATTGC 64
Db 780 GTGATAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTTGAACGCACATTGC 721
Qy 65 GCGCGCCAGTAATCTCGCGGGCATGCTGTTGAGCGTCAATTTCAACCCCTCAAGCCCGCC 124
Db 720 GCGCGCCAGTAATCTCGCGGGCATGCTGTTGAGCGTCAATTTCAACCCCTCAAGCCCGCC 661
Qy 125 GGTTCGTGTTGGGATCGCAAGCCCTTTCGCGCAAGCCCGCCCGAAATCTAGTGGCG 184
Db 660 G-----CTTGGTGTGGGAGCTGCAGTCTCTGCTCCCTCCCAAAATATACATTGCGG 608
Qy 185 TCTCGCTGCAGCTTCCATTGCGTAGTAGTAAACCCCTCGCAACTGGTAGCGCGCGCGCC 244
Db 607 TCACTGCGAGCTTCCCATAGCGTAGTAATTTACATCGTACTGTTAATCGTCGCGGCC 548
Qy 245 AAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCCGCTGA 304
Db 547 ACGCCGTTAAA-CCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCCGCTGA 489
Qy 305 ACTTAA 310
Db 488 ACTTAA 483

RESULT 15
US-09-961-755A-6
; Sequence 6, Application US/09961755A
; Publication No. US2003011372A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Gibberella zeae
US-09-961-755A-6

Query Match 57.8%; Score 179.2; DB 10; Length 521;
Best Local Similarity 83.3%; Pred. No. 1.8e-54;
Matches 255; Conservative 0; Mismatches 38; Indels 13; Gaps 4;

Qy 1 AAATGCCATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTTGAACGCACA 60
Db 229 AAATGCCATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTTGAACGCACA 288
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QY 61 TTGCGCCCGCCAGTATTCTGGCGGCATGCTGTTGAGCGTCAATTTCAACCCCTCAAGCC 120
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 Db 289 TTGCGCCCGCCAGTATTCTGGCGGCATGCTGTTGAGCGTCAATTTCAACCCCTCAAGCC 348
 |||||
 QY 121 CCCGGGTTTGGTGTGGGATCGGCAAGCCCTTGGCGCAAGCCGCGCCCGGAATCTAGTG 180
 |||||
 Db 349 C---AGCTTGGTGTGGG-----AGCTGCACTCTGCTGCACTCCCCAAATACATTG 397
 |||||
 QY 181 GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAACCTCGCAACTGGTACGCGCGC 240
 |||||
 Db 398 GCGGTCAAG-TGAGCTTCCATAGCGTAGTAATTACACATCGTTACTGGTAATCGTCG 456
 |||||
 QY 241 GGCCAAAGCGTTAAACCCCAACTTCTGAATGTGACCTCGGATCAGGTAGGAATACCCG 300
 |||||
 Db 457 GGCCAGCGCGTTAAA-CCCAACTTCTGAATGTGACCTCGGATCAGGTAGGAATACCCG 515
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 QY 301 CTGAAC 306
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 Db 516 CTGAAC 521

Search completed: October 23, 2005, 23:48:15
 Job time : 1340.32 secs

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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 06:56:31 ; Search time 10.7318 Seconds
(without alignments)
2744.464 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18
Sequence: 1 tctagtgcggtctcgct 18

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3 US-09-423-233-49	Sequence 49, Appl
2	16.4	91.1	310	3 US-09-423-233-7	Sequence 7, Appl
3	16.4	91.1	583	1 US-08-652-127C-8	Sequence 8, Appl
4	16.4	91.1	594	1 US-08-652-127C-5	Sequence 5, Appl
5	16.4	91.1	2293	3 US-09-645-073-1	Sequence 1, Appl
6	14.8	82.2	531	1 US-08-652-127C-7	Sequence 7, Appl
7	14.8	82.2	581	1 US-08-652-127C-6	Sequence 6, Appl
8	14.8	82.2	15163	4 US-09-949-016-13246	Sequence 13246, A
9	14.8	82.2	39376	4 US-09-949-016-17536	Sequence 17536, A
10	14.8	82.2	63982	4 US-09-949-016-16769	Sequence 16769, A
11	14.4	80.0	601	4 US-09-949-016-54231	Sequence 54231, A
12	14.4	80.0	945	4 US-09-710-279-3309	Sequence 3309, Ap
13	14.4	80.0	1146	4 US-09-710-279-3055	Sequence 3055, Ap
14	14.4	80.0	1629	4 US-09-252-991A-2042	Sequence 2042, Ap
15	14.4	80.0	1308	4 US-09-252-991A-1914	Sequence 1914, Ap
16	14.4	80.0	2382	4 US-09-710-279-3385	Sequence 3385, Ap
17	14.4	80.0	3116	4 US-09-710-279-4248	Sequence 4248, Ap
18	14.4	80.0	9676	4 US-09-949-016-16629	Sequence 16629, A
19	14.4	80.0	46899	1 US-08-471-119A-1	Sequence 1, Appl
20	14	77.8	636	2 US-08-737-129A-1	Sequence 1, Appl
21	14	77.8	639	3 US-09-170-769A-1	Sequence 1, Appl
22	14	77.8	645	3 US-09-170-769A-5	Sequence 5, Appl
23	14	77.8	666	2 US-08-737-129A-5	Sequence 5, Appl
24	14	77.8	717	5 PCT-US94-14106-58	Sequence 58, Appl
25	14	77.8	735	5 PCT-US94-14106-50	Sequence 50, Appl
26	14	77.8	735	5 PCT-US94-14106-54	Sequence 54, Appl
27	14	77.8	777	2 US-08-860-882A-25	Sequence 25, Appl

C 28	14	77.8	777	3	US-09-011-769A-20	Sequence 20, Appl
C 29	14	77.8	798	1	US-08-133-011-99	Sequence 99, Appl
C 30	14	77.8	798	1	US-08-322-730A-99	Sequence 99, Appl
C 31	14	77.8	798	1	US-08-387-874-71	Sequence 71, Appl
C 32	14	77.8	798	2	US-08-383-619-99	Sequence 99, Appl
C 33	14	77.8	798	3	US-08-907-739-99	Sequence 99, Appl
C 34	14	77.8	798	3	US-09-729-597-99	Sequence 99, Appl
C 35	14	77.8	798	5	PCT-US93-08364-71	Sequence 71, Appl
C 36	14	77.8	830	1	US-08-133-011-115	Sequence 115, App
C 37	14	77.8	830	1	US-08-322-730A-115	Sequence 115, App
C 38	14	77.8	830	2	US-08-387-874-88	Sequence 88, Appl
C 39	14	77.8	830	2	US-08-383-619-115	Sequence 115, App
C 40	14	77.8	830	3	US-08-907-739-115	Sequence 115, App
C 41	14	77.8	830	3	US-09-729-597-115	Sequence 115, App
C 42	14	77.8	830	5	PCT-US93-08364-88	Sequence 88, Appl
C 43	14	77.8	923	5	PCT-US94-07659-1	Sequence 1, Appl
C 44	14	77.8	1056	4	US-10-134-188-30	Sequence 30, Appl
C 45	14	77.8	1077	4	US-09-489-039A-1514	Sequence 1514, Ap

ALIGNMENTS

RESULT 1
US-09-423-233-49
; Sequence 49, Application US/09423233
; Patent No. 6372430
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 03063-0341WP
; CURRENT APPLICATION NUMBER: US/09423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-09-423-233-49

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGTGACGGTCTCGCT 18
DB 1 TCTAGTGACGGTCTCGCT 18

RESULT 2
US-09-423-233-7
; Sequence 7, Application US/09423233
; Patent No. 6372430
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 03063-0341WP
; CURRENT APPLICATION NUMBER: US/09423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-09-423-233-7

Query Match 91.1%; Score 16.4; DB 3; Length 310;
Best Local Similarity 94.4%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 TCTAGTGACGGTCTCGCT 18
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Db      174 TCTAGTGGCGGTCTCGCT 191

RESULT 3
US-08-652-127C-8
; Sequence 8, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-8

Query Match          91.1%; Score 16.4; DB 1; Length 583;
Best Local Similarity 94.4%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TCTAGTGACGGTCTCGCT 18
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Db      429 TCTAGTGGCGGTCTCGCT 446

RESULT 4
US-08-652-127C-5
; Sequence 5, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-8

Query Match          91.1%; Score 16.4; DB 1; Length 583;
Best Local Similarity 94.4%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TCTAGTGACGGTCTCGCT 18
      |||||
Db      429 TCTAGTGGCGGTCTCGCT 446

RESULT 5
US-09-645-073-1
; Sequence 1, Application US/09645073
; Patent No. 6287800
; GENERAL INFORMATION:
; APPLICANT: Lee, May
; APPLICANT: Galazzo, Jorge
; TITLE OF INVENTION: Production of High Titers of Gibberellins GA4 and GA7
; FILE REFERENCE: L02-01NP
; CURRENT APPLICATION NUMBER: US/09/645,073
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,770
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: Gibberella fujikuroi
; US-09-645-073-1

Query Match          91.1%; Score 16.4; DB 3; Length 2293;
Best Local Similarity 94.4%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TCTAGTGACGGTCTCGCT 18
      |||||
Db      2145 TCTAGTGGCGGTCTCGCT 2162

RESULT 6
US-08-652-127C-7
; Sequence 7, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 594
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-5

Query Match          91.1%; Score 16.4; DB 1; Length 594;
Best Local Similarity 94.4%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 531
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-7

Query Match 82.2%; Score 14.8; DB 1; Length 531;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCTAGTGACGGTCTCGCT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 377 TATAGTGGCGGTCTCGCT 394

RESULT 7
US-08-652-127C-6
Sequence 6, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
ADDRESS: Seaby & MacLean
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 581
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-6
Query Match 82.2%; Score 14.8; DB 1; Length 581;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TCTAGTGACGGTCTCGCT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 427 TATAGTGGCGGTCTCGCT 444
RESULT 8
US-09-949-016-13246
Sequence 13246, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13246
LENGTH: 15163
TYPE: DNA
ORGANISM: Human
US-09-949-016-13246

Query Match 82.2%; Score 14.8; DB 4; Length 15163;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TCTAGTGACGGTCTCGCT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 5781 TTTAGAGACGGTCTCGCT 5798

RESULT 9
US-09-949-016-17536/c
Sequence 17536, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17536
LENGTH: 39376
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(39376)

```
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17536

Query Match      82.2%; Score 14.8; DB 4; Length 39376;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCTAGTGACGGTCTCGCT 18
    ||||| | |||||
Db 6959 TCTAGTGGCTCTCGCT 6942

RESULT 10
US-09-949-016-16769
; Sequence 16769, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16769
; LENGTH: 63982
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16769

Query Match      82.2%; Score 14.8; DB 4; Length 63982;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCTAGTGACGGTCTCGCT 18
    ||||| | |||||
Db 19046 TCTAGTACTGTCTCAT 19063

RESULT 11
US-09-949-016-54231/c
; Sequence 54231, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54231
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016--54231

Query Match      80.0%; Score 14.4; DB 4; Length 601;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
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```
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCTAGTGACGGTCTCGCT 18
    ||||| | |||||
Db 314 TTTAGAGACGGTCYCGCT 297

RESULT 12
US-09-710-279-3309/c
; Sequence 3309, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3309
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3309

Query Match      80.0%; Score 14.4; DB 4; Length 945;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTAGTGACGGTCTCGC 17
    ||||| | |||||
Db 268 CTACTGACGGTCTCGC 253

RESULT 13
US-09-710-279-3055/c
; Sequence 3055, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3055
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3055

Query Match      80.0%; Score 14.4; DB 4; Length 1146;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTAGTGACGGTCTCGC 17
    ||||| | |||||
Db 469 CTACTGACGGTCTCGC 454

RESULT 14
US-09-252-991A-2042
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; Sequence 2042, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2042
; LENGTH: 1629
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2042

Query Match 80.0%; Score 14.4; DB 4; Length 1629;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TAGTGACGGTCTCGCT 18
|| |||||
Db 440 TACTGACGGTCTCGCT 455

RESULT 15
US-09-252-991A-1914/c
; Sequence 1914, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1914
; LENGTH: 1908
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1914

Query Match 80.0%; Score 14.4; DB 4; Length 1908;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TAGTGACGGTCTCGCT 18
|| |||||
Db 1286 TACTGACGGTCTCGCT 1271

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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 15:20:46 ; Search time 77.8251 Seconds
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Title: US-10-046-955-49

Perfect score: 18

Sequence: 1 tctagtacggtctcgct 18

Scoring table: IDENTITY NUC

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Searched: 9772231 seqs, 4124568258 residues

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Listing first 45 summaries

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- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	15	US-10-046-955-49
2	16.4	91.1	310	15	US-10-046-955-7
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4	16.4	91.1	534	20	US-10-773-904-7
5	16.4	91.1	534	20	US-10-773-905-7
6	15.4	85.6	279	20	US-10-425-115-131520
7	15	83.3	386	10	US-09-918-995-33508

c	8	15	83.3	449	10	US-09-918-995-34287	Sequence 34287, A
c	9	15	83.3	473	10	US-09-918-995-1024	Sequence 1024, Ap
c	10	15	83.3	1596	22	US-10-450-763-24124	Sequence 24124, A
c	11	15	83.3	1620	20	US-10-684-422-237	Sequence 237, App
c	12	14.8	82.2	25	24	US-11-036-317-568242	Sequence 568242, A
c	13	14.8	82.2	388	18	US-10-424-599-44516	Sequence 44516, A
c	14	14.8	82.2	403	20	US-10-357-930-2782	Sequence 2782, Ap
c	15	14.8	82.2	558	19	US-10-437-963-74582	Sequence 74582, A
c	16	14.8	82.2	599	13	US-10-027-632-215234	Sequence 215234, A
c	17	14.8	82.2	599	13	US-10-027-632-215235	Sequence 215235, A
c	18	14.8	82.2	599	17	US-10-027-632-215234	Sequence 215234, A
c	19	14.8	82.2	599	17	US-10-027-632-215235	Sequence 215235, A
c	20	14.8	82.2	675	19	US-10-767-701-8208	Sequence 8208, Ap
c	21	14.8	82.2	695	20	US-10-425-115-42609	Sequence 42609, A
c	22	14.8	82.2	1090	12	US-09-925-065A-35831	Sequence 35831, A
c	23	14.8	82.2	1090	12	US-09-925-065A-35832	Sequence 35832, A
c	24	14.8	82.2	1113	12	US-09-925-065A-37892	Sequence 37892, A
c	25	14.8	82.2	2231	12	US-09-925-065A-680442	Sequence 680442, A
c	26	14.8	82.2	3461	19	US-10-437-963-82321	Sequence 82321, A
c	27	14.8	82.2	23606	21	US-10-741-600-17944	Sequence 17944, A
c	28	14.8	82.2	28573	19	US-10-741-601-5769	Sequence 5769, Ap
c	29	14.8	82.2	37305	20	US-10-719-993-6767	Sequence 6767, Ap
c	30	14.8	82.2	60500	13	US-10-087-192-1024	Sequence 1024, Ap
c	31	14.8	82.2	60615	19	US-10-633-423-9	Sequence 9, Appli
c	32	14.8	82.2	60615	19	US-10-427-741-9	Sequence 9, Appli
c	33	14.8	82.2	75839	13	US-10-087-192-166	Sequence 166, App
c	34	14.8	82.2	198285	9	US-09-880-107-3814	Sequence 3814, Ap
c	35	14.8	82.2	198285	19	US-10-775-169-338	Sequence 338, App
c	36	14.8	82.2	198285	22	US-10-756-149-12	Sequence 12, Appl
c	37	14.4	80.0	25	21	US-10-719-900-912120	Sequence 912120, A
c	38	14.4	80.0	601	20	US-10-425-115-128972	Sequence 128972, A
c	39	14	77.8	25	21	US-10-719-900-176089	Sequence 176089, A
c	40	14	77.8	70	22	US-10-516-429-20	Sequence 20, Appl
c	41	14	77.8	479	9	US-09-864-761-25477	Sequence 25477, A
c	42	14	77.8	489	18	US-10-276-774-270	Sequence 270, App
c	43	14	77.8	502	12	US-09-925-065A-406631	Sequence 406631, A
c	44	14	77.8	502	12	US-09-925-065A-406632	Sequence 406632, A
c	45	14	77.8	550	9	US-09-864-761-8809	Sequence 8809, Ap

ALIGNMENTS

RESULT 1
US-10-046-955-49
; Sequence 49, Application US/10046955
; Publication No. US20030129600A1

; GENERAL INFORMATION:

; APPLICANT: The Government of the United States of America, as Represented by the

; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis

; APPLICANT: Control and Prevention

; APPLICANT: Morrison, Christine J.

; APPLICANT: Reiss, Errol

; APPLICANT: Aidorevich, Liliana

; APPLICANT: Choi, Jong Soo

; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and

; TITLE OF INVENTION: Other Filamentous Fungi

; FILE REFERENCE: 6395-62064

; CURRENT APPLICATION NUMBER: US/10/046,955

; CURRENT FILING DATE: 2002-06-04

; PRIOR APPLICATION NUMBER: US 09/423,233

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: PCT/US98/08926

; PRIOR FILING DATE: 1998-05-01

; PRIOR APPLICATION NUMBER: US 60/045,400

; PRIOR FILING DATE: 1997-05-02

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 49

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Fusarium moniliforme

US-10-046-955-49

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Query Match      100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTAGTGACGGTCTCGCT 18
    ||||| ||||| |||||
Db 1 TCTAGTGACGGTCTCGCT 18

RESULT 2
US-10-046-955-7
; Sequence 7, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Liliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; TITLE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-10-046-955-7

Query Match      91.1%; Score 16.4; DB 15; Length 310;
Best Local Similarity 94.4%; Pred. No. 85;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCTAGTGACGGTCTCGCT 18
    ||||| ||||| |||||
Db 174 TCTAGTGGCGTCTCGCT 191

RESULT 3
US-09-961-755A-7
; Sequence 7, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7

Query Match      91.1%; Score 16.4; DB 10; Length 534;
Best Local Similarity 94.4%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCTAGTGACGGTCTCGCT 18
    ||||| ||||| |||||
Db 1 TCTAGTGACGGTCTCGCT 18

RESULT 4
US-10-773-904-7
; Sequence 7, Application US/10773904
; Publication No. US20040259120A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/10/773,904
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/09/961,755
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-10-773-904-7

Query Match      91.1%; Score 16.4; DB 20; Length 534;
Best Local Similarity 94.4%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCTAGTGACGGTCTCGCT 18
    ||||| ||||| |||||
Db 402 TCTAGTGGCGGTCTCGCT 419

RESULT 5
US-10-773-905-7
; Sequence 7, Application US/10773905
; Publication No. US20040259121A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/10/773,905
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/09/961,755
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-10-773-905-7

Query Match      91.1%; Score 16.4; DB 20; Length 534;
Best Local Similarity 94.4%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCTAGTGACGGTCTCGCT 18
    ||||| ||||| |||||
Db 402 TCTAGTGGCGGTCTCGCT 419

RESULT 6
US-10-425-115-131520
; Sequence 131520, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
```



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/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 131520
/ LENGTH: 279
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_51429C.1
US-10-425-115-131520

Query Match      85.6%; Score 15.4; DB 20; Length 279;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTAGTACGGTCTCGCT 18
Db      82 CGAGTGACGGTCTCGCT 98

RESULT 7
US-09-918-995-33508/c
/ Sequence 33508, Application US/09918995
/ Publication No. US20030073623A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
/ FILE REFERENCE: 20411-756
/ CURRENT APPLICATION NUMBER: US/09/918,995
/ CURRENT FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: US/09/235,076
/ PRIOR FILING DATE: 1999-01-20
/ NUMBER OF SEQ ID NOS: 38054
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 33508
/ LENGTH: 386
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-918-995-33508

Query Match      83.3%; Score 15; DB 10; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 AGTGACGGTCTCGCT 18
Db      208 AGTGACGGTCTCGCT 194

RESULT 8
US-09-918-995-34287/c
/ Sequence 34287, Application US/09918995
/ Publication No. US20030073623A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
/ FILE REFERENCE: 20411-756
/ CURRENT APPLICATION NUMBER: US/09/918,995
/ CURRENT FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: US/09/235,076
/ PRIOR FILING DATE: 1999-01-20
/ NUMBER OF SEQ ID NOS: 38054
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 34287
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```
/ LENGTH: 449
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)...(449)
/ OTHER INFORMATION: n = A,T,C or G
US-09-918-995-34287

Query Match      83.3%; Score 15; DB 10; Length 449;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 AGTGACGGTCTCGCT 18
Db      253 AGTGACGGTCTCGCT 239

RESULT 9
US-09-918-995-1024/c
/ Sequence 1024, Application US/09918995
/ Publication No. US20030073623A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
/ FILE REFERENCE: 20411-756
/ CURRENT APPLICATION NUMBER: US/09/918,995
/ CURRENT FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: US/09/235,076
/ PRIOR FILING DATE: 1999-01-20
/ NUMBER OF SEQ ID NOS: 38054
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1024
/ LENGTH: 473
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)...(473)
/ OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1024

Query Match      83.3%; Score 15; DB 10; Length 473;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 AGTGACGGTCTCGCT 18
Db      230 AGTGACGGTCTCGCT 216

RESULT 10
US-10-450-763-24124
/ Sequence 24124, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790CIP3/US
/ CURRENT APPLICATION NUMBER: US/10/450,763
/ CURRENT FILING DATE: 2003-06-11
/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO 24124
/ LENGTH: 1596
/ TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1416)..(1033)
; OTHER INFORMATION: 64% homologous to Homo sapiens HCG V, accession number
; OTHER INFORMATION: US5388,Smith-Waterman Score=380.
US-10-450-763-24124

Query Match      83.3%; Score 15; DB 20; Length 1596;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 AGTGACGGTCTCGCT 18
      |||||
Db     1378 AGTGACGGTCTCGCT 1392

RESULT 11
US-10-684-422-237/c
; Sequence 237, Application US/10684422
; Publication No. US20040229233A1
; GENERAL INFORMATION:
; APPLICANT: ABURATANI, Hiroyuki
; APPLICANT: YAMAMOTO, Shogo
; TITLE OF INVENTION: Human housekeeping genes and human tissue-specific genes
; FILE REFERENCE: 113991
; CURRENT APPLICATION NUMBER: US/10/684,422
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/416,614
; PRIOR FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 332
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 237
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (200)..(580)
US-10-684-422-237

Query Match      83.3%; Score 15; DB 20; Length 1620;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 AGTGACGGTCTCGCT 18
      |||||
Db     238 AGTGACGGTCTCGCT 224

RESULT 12
US-11-036-317-568242/c
; Sequence 568242, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 568242
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
;
US-11-036-317-568242

Query Match      82.2%; Score 14.8; DB 24; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TCTAGTGACGGTCTCGCT 18
      |||||
Db     19 TCGAGTGAAGGTCTCGCT 2

RESULT 13
US-10-424-599-44516
; Sequence 44516, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 44516
; LENGTH: 388
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_140197C.1
US-10-424-599-44516

Query Match      82.2%; Score 14.8; DB 18; Length 388;
Best Local Similarity 88.9%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TCTAGTGACGGTCTCGCT 18
      |||||
Db     319 TTACTGACGGTCTCGCT 336

RESULT 14
US-10-357-930-2782/c
; Sequence 2782, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2782
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
;

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 211, 216, 362, 364
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-2782

Query Match      82.2%; Score 14.8; DB 20; Length 403;
Best Local Similarity 88.9%; Pred. NO. 6.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TCTAGTGACGGTCTCGCT 18
        |||||
Db      350 TCTAGTGACGGTCTCGCT 333

RESULT 15
US-10-437-963-74582/c
; Sequence 74582, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 74582
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_74754C.1
US-10-437-963-74582

Query Match      82.2%; Score 14.8; DB 19; Length 558;
Best Local Similarity 88.9%; Pred. NO. 6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TCTAGTGACGGTCTCGCT 18
        |||||
Db      504 TCTAGAGACGGTCACGCT 487
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Job time : 79.8251 secs

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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 06:56:31 ; Search time 10.7318 Seconds
(without alignments)
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Title: US-10-046-955-50
Perfect score: 18
Sequence: 1 cgttaattcgcttcttc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/prodata/1/ina/PCUS COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	US-09-423-233-50
2	15	83.3	615	4	US-09-134-000C-314
3	14.8	82.2	207	4	US-09-107-532A-1902
4	14.8	82.2	650	4	US-09-669-751-103
5	14.8	82.2	2457	4	US-09-134-000C-2950
6	14.4	80.0	939	4	US-09-710-279-3059
7	14.4	80.0	963	3	US-09-134-000C-1367
8	14.4	80.0	2815	4	US-09-710-279-3819
9	14.4	80.0	146401	4	US-09-949-016-16151
10	14	77.8	3208	1	US-07-972-791-3
11	14	77.8	3345	1	US-07-972-791-7
12	14	77.8	3346	1	US-07-972-791-5
13	14	77.8	3347	1	US-07-972-791-2
14	14	77.8	3347	1	US-07-972-791-8
15	14	77.8	3361	1	US-07-972-791-6
16	14	77.8	3434	6	5310649-1
17	14	77.8	3434	6	5310649-1
18	13.8	76.7	601	4	US-09-949-016-142005
19	13.8	76.7	601	4	US-09-949-016-142006
20	13.8	76.7	601	4	US-09-949-016-172751
21	13.8	76.7	702	4	US-09-543-681A-4125
22	13.8	76.7	1356	4	US-09-328-352-1886
23	13.8	76.7	1386	3	US-09-134-001C-984
24	13.8	76.7	2229	4	US-09-902-540-4193
25	13.8	76.7	5679	3	US-08-844-274-10
26	13.8	76.7	5679	4	US-09-598-421-10
27	13.8	76.7	6642	4	US-09-809-665A-80

c	28	13.8	76.7	6723	3	US-08-844-274-13	Sequence 13, Appl
c	29	13.8	76.7	6723	3	US-08-844-274-14	Sequence 14, Appl
c	30	13.8	76.7	6723	4	US-09-598-421-13	Sequence 13, Appl
c	31	13.8	76.7	6723	4	US-09-598-421-14	Sequence 14, Appl
c	32	13.8	76.7	7560	3	US-08-844-274-20	Sequence 20, Appl
c	33	13.8	76.7	7560	4	US-09-598-421-20	Sequence 20, Appl
c	34	13.8	76.7	9423	4	US-09-377-066-6	Sequence 6, Appl
c	35	13.8	76.7	9676	4	US-09-949-016-16629	Sequence 16629, A
c	36	13.8	76.7	9704	3	US-09-814-951A-3	Sequence 3, Appl
c	37	13.8	76.7	9717	3	US-09-251-645-1	Sequence 1, Appl
c	38	13.8	76.7	9805	4	US-09-949-016-16862	Sequence 16862, A
c	39	13.8	76.7	12866	3	US-08-961-527-137	Sequence 137, App
c	40	13.8	76.7	21330	4	US-09-902-540-1209	Sequence 1209, Ap
c	41	13.8	76.7	46492	4	US-09-949-016-12953	Sequence 12953, A
c	42	13.8	76.7	46492	4	US-09-949-016-12954	Sequence 12954, A
c	43	13.8	76.7	49795	3	US-09-453-702B-60	Sequence 60, Appl
c	44	13.8	76.7	61847	3	US-09-949-016-16677	Sequence 16677, A
c	45	13.8	76.7	75674	4	US-09-949-016-17597	Sequence 17597, A

ALIGNMENTS

RESULT 1

US-09-423-233-50
; Sequence 50, Application US/09423233
; Patent No. 6372430
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341WP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 50
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Fusarium oxysporum
US-09-423-233-50

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CGTTAATTCGCTTCTC 18
Db	1	CGTTAATTCGCTTCTC 18

RESULT 2

US-09-134-000C-314
; Sequence 314, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 314
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-314

Query Match 83.3%; Score 15; DB 4; Length 615;

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCGTTCC 16
Db 172 GTTAATTCGCGTTCC 186

RESULT 3
US-09-107-532A-1902/c
; Sequence 1902, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1902:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...207
; SEQUENCE DESCRIPTION: SEQ ID NO: 1902:
US-09-107-532A-1902

Query Match 82.2%; Score 14.8; DB 4; Length 207;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCCTC 18
Db 84 CGTTAATTCGTTCCCTC 67

RESULT 4
US-09-669-751-103
; Sequence 103, Application US/09669751
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; Patent No. 6551575
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; TITLE OF INVENTION: Methods for Identifying Compounds for
; Motion Sickness, Vertigo and Other Disorders Related to
; TITLE OF INVENTION: Balance and the Perception of Gravity
; FILE REFERENCE: P-NI 3864
; CURRENT APPLICATION NUMBER: US/09/669,751
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/168,579
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Drosophila
US-09-669-751-103

Query Match 82.2%; Score 14.8; DB 4; Length 650;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCCTC 18
Db 69 CGTTCATACGCGTTCCCTC 86

RESULT 5
US-09-134-000C-2950/c
; Sequence 2950, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2950
; LENGTH: 2457
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2950

Query Match 82.2%; Score 14.8; DB 4; Length 2457;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCCTC 18
Db 963 CGTTAATTCGCGTTCCGC 946

RESULT 6
US-09-710-279-3059/c
; Sequence 3059, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/184,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3059
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; LENGTH: 939
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3059

Query Match      80.0%; Score 14.4; DB 4; Length 939;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TTAATTCGCGTTCCTC 18
        ||||| |||||
Db      792 TTAATTCAGTTCCTC 807

RESULT 9
US-09-949-016-16151
; Sequence 16151, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16151
; LENGTH: 146401
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16151

Query Match      80.0%; Score 14.4; DB 4; Length 146401;
Best Local Similarity 93.8%; Pred. No. 3.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TTAATTCGCGTTCCTC 18
        ||||| |||||
Db      89697 TTAATTCGTTTCCTC 89712

RESULT 10
US-07-972-791-3/c
; Sequence 3, Application US/07972791
; Patent No. 5348857
; GENERAL INFORMATION:
; APPLICANT: Ficht, Thomas A.
; APPLICANT: Sowa, Blair A.
; APPLICANT: Adams, L. Gary
; TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
; TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,791
; FILING DATE: 19921106
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettelberger, Denise M.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
```

```
;
;
; TELEX: 792026
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3208 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Brucella abortus
; STRAIN: biovar 1 (s2308)
US-07-972-791-3

Query Match 77.8%; Score 14; DB 1; Length 3208;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCGTTC 15
|||||
Db 1488 GTTAATTCGCGTTC 1475

RESULT 11
US-07-972-791-7/c
; Sequence 7, Application US/07972791
; Patent No. 5348857
; GENERAL INFORMATION:
; APPLICANT: Ficht, Thomas A.
; APPLICANT: Sowa, Blair A.
; APPLICANT: Adams, L. Gary
; TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
; TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19921106
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettelberger, Denise M.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; TELEX: 792026
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3346 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Brucella neotomae
;
US-07-972-791-5

Query Match 77.8%; Score 14; DB 1; Length 3346;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCGTTC 15
|||||
Db 1488 GTTAATTCGCGTTC 1475

RESULT 13
US-07-972-791-2/c
; Sequence 2, Application US/07972791
; Patent No. 5348857
; GENERAL INFORMATION:
; APPLICANT: Ficht, Thomas A.
; APPLICANT: Sowa, Blair A.
; APPLICANT: Adams, L. Gary
; TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
; TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
;
US-07-972-791-7

Query Match 77.8%; Score 14; DB 1; Length 3345;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCGTTC 15
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```

; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Brucella suis
; STRAIN: biovar 1
US-07-972-791-8

Query Match 77.8%; Score 14; DB 1; Length 3347;
Best Local Similarity 100.0%; Pred. NO. 4.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0

QY 2 GTTAATTCGCGTTC 15
      |||||
DB 1488 GTTAATTCGCGTTC 1475

RESULT 15
US-07-972-791-6/c
; Sequence 6, Application US/07972791
; Patent No. 5348857
; GENERAL INFORMATION:
; APPLICANT: Ficht, Thomas A.
; APPLICANT: Sowa, Blair A.
; APPLICANT: Adams, L. Gary
; TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
; TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: Texas
; COUNTRY: USA

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3361 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella ovis
US-07-972-791-6

Query Match 77.8%; Score 14; DB 1; Length 3361;
Best Local Similarity 100.0%; Pred.No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels

QY 2 GTTAATTCGCGTTC 15
Db 1503 GTTAATTCGCGTTC 1490
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|||||

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Job time : 11.7318 secs

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Search completed: October 23, 2005, 16:07:08
Job time : 11.7318 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 15:20:46 ; Search time 77.8251 Seconds
(without alignments)
1907.926 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaattcggtcttc 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9772231 seqs, 4124568258 residues

Total number of hits satisfying chosen parameters: 19544462

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	15	US-10-046-955-50
2	15.4	85.6	538	20	Sequence 50, Appl
3	15.4	85.6	538	20	Sequence 23645, A
4	15.4	85.6	538	21	Sequence 23646, A
5	15.4	85.6	538	21	Sequence 23645, A
6	15.4	85.6	4461	19	Sequence 23646, A
7	15	83.3	127	17	Sequence 93618, A

c	8	15	83.3	128	9	US-09-815-242-996	Sequence 996, App
c	9	15	83.3	250	9	US-09-815-242-555	Sequence 555, App
c	10	15	83.3	250	17	US-10-282-122A-531	Sequence 531, App
c	11	15	83.3	1467	17	US-10-282-122A-6332	Sequence 6332, App
c	12	15	83.3	9212	9	US-09-070-927A-334	Sequence 334, App
c	13	14.8	82.2	262	10	US-09-535-459-1371	Sequence 1371, App
c	14	14.8	82.2	438	18	US-10-424-599-43896	Sequence 43896, A
c	15	14.8	82.2	554	20	US-10-363-345A-1073	Sequence 1073, App
c	16	14.8	82.2	554	20	US-10-363-345A-1074	Sequence 1074, App
c	17	14.8	82.2	554	21	US-10-363-483A-1073	Sequence 1073, App
c	18	14.8	82.2	554	21	US-10-363-483A-1074	Sequence 1074, App
c	19	14.8	82.2	585	19	US-10-437-963-81762	Sequence 81762, A
c	20	14.8	82.2	650	14	US-10-255-536-103	Sequence 103, App
c	21	14.8	82.2	816	20	US-10-425-115-60210	Sequence 60210, A
c	22	14.8	82.2	1200	24	US-11-097-143-16178	Sequence 16178, A
c	23	14.8	82.2	1231	20	US-10-363-345A-14681	Sequence 14681, A
c	24	14.8	82.2	1231	20	US-10-363-345A-14682	Sequence 14682, A
c	25	14.8	82.2	1231	21	US-10-363-483A-14681	Sequence 14681, A
c	26	14.8	82.2	1231	21	US-10-363-483A-14682	Sequence 14682, A
c	27	14.8	82.2	1445	20	US-10-425-115-145901	Sequence 145901, A
c	28	14.8	82.2	3135	17	US-10-282-122A-20853	Sequence 20853, A
c	29	14.8	82.2	3138	9	US-09-815-242-6520	Sequence 6520, App
c	30	14.8	82.2	3257	24	US-11-097-143-16177	Sequence 16177, A
c	31	14.8	82.2	4491	24	US-11-097-143-316	Sequence 316, App
c	32	14.8	82.2	5864	24	US-11-097-143-2872	Sequence 1279, App
c	33	14.8	82.2	15428	24	US-11-097-143-1279	Sequence 1279, App
c	34	14.8	82.2	2731748	19	US-10-297-465A-1	Sequence 1, Appli
c	35	14.4	80.0	65	16	US-10-032-585-259	Sequence 259, App
c	36	14.4	80.0	230	17	US-10-242-535A-247	Sequence 247, App
c	37	14.4	80.0	230	18	US-10-085-783A-247	Sequence 247, App
c	38	14.4	80.0	306	9	US-09-974-300-6603	Sequence 6603, App
c	39	14.4	80.0	467	12	US-09-925-065A-400752	Sequence 400752, A
c	40	14.4	80.0	536	12	US-09-925-065A-18369	Sequence 18369, A
c	41	14.4	80.0	540	20	US-10-363-345A-4913	Sequence 4913, App
c	42	14.4	80.0	540	20	US-10-363-345A-4914	Sequence 4914, App
c	43	14.4	80.0	540	21	US-10-363-483A-4913	Sequence 4913, App
c	44	14.4	80.0	540	21	US-10-363-483A-4914	Sequence 4914, App
c	45	14.4	80.0	559	16	US-10-029-386-7594	Sequence 7594, App

ALIGNMENTS

RESULT 1

US-10-046-955-50
; Sequence 50, Application US/10046955
; Publication No. US20030129600A1

GENERAL INFORMATION:

; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Di:
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aldorevich, Liliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; TITLE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Fusarium oxysporum
US-10-046-955-50

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Query Match      100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CGTTAATTCCGGTTCCTC 18
        |||||
Db      1 CGTTAATTCCGGTTCCTC 18

RESULT 2
US-10-363-345A-23645
; Sequence 23645, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 23645
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-23645

Query Match      85.6%; Score 15.4; DB 20; Length 538;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GTTAATTCCGGTTCCTC 18
        |||||
Db      434 GTTAATTCCGGTTCGTC 450

RESULT 3
US-10-363-345A-23646/c
; Sequence 23646, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 23646
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-23646

Query Match      85.6%; Score 15.4; DB 20; Length 538;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GTTAATTCCGGTTCCTC 18
        |||||
Db      105 GTTAATTCCGGTTCGTC 89
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RESULT 4
US-10-363-483A-23645
; Sequence 23645, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 23645
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-483A-23645

Query Match      85.6%; Score 15.4; DB 21; Length 538;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GTTAATTCCGGTTCCTC 18
        |||||
Db      434 GTTAATTCCGGTTCGTC 450
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```
RESULT 5
US-10-363-483A-23646/c
; Sequence 23646, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 23646
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-483A-23646

Query Match      85.6%; Score 15.4; DB 21; Length 538;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GTTAATTCCGGTTCCTC 18
        |||||
Db      105 GTTAATTCCGGTTCGTC 89
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```
RESULT 6
US-10-437-963-93618/c
; Sequence 93618, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
```

```
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 93618
; LENGTH: 4461
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_91986C.1
US-10-437-963-93618

Query Match      85.6%; Score 15.4; DB 19; Length 4461;
Best Local Similarity 94.1%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GTTAATTCGGTTCCTC 18
DB      1209 GTTAATTCAGTTCCTC 1193

RESULT 7
US-10-282-122A-978/c
; Sequence 978, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 978
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; LENGTH: 127
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-978

Query Match      83.3%; Score 15; DB 17; Length 127;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTAATTCGGTTCC 16
DB      117 GTTAATTCGGTTCC 103

RESULT 8
US-09-815-242-996/c
; Sequence 996, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 996
; LENGTH: 128
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-996

Query Match      83.3%; Score 15; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTAATTCGGTTCC 16
DB      118 GTTAATTCGGTTCC 104

RESULT 9
US-09-815-242-555/c
; Sequence 555, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
```

```
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 555
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-555

Query Match      83.3%; Score 15; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GTTAATTGCGGTTC 16
Db      54 GTTAATTGCGGTTC 40

RESULT 10
US-10-282-122A-531/c
; Sequence 531, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zvekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6332
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
```

```
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 531
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-531

Query Match      83.3%; Score 15; DB 17; Length 250;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GTTAATTGCGGTTC 16
Db      54 GTTAATTGCGGTTC 40

RESULT 11
US-10-282-122A-6332
; Sequence 6332, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zvekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6332
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
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US-10-282-122A-6332

Query Match 83.3%; Score 15; DB 17; Length 1467;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGGTTC 16
DB 1027 GTTAATTCGGTTC 1041

RESULT 12

US-09-070-927A-334
; Sequence 334, Application US/09070927A
; Patent No. US20020120116A1

GENERAL INFORMATION:

APPLICANT: Charles A. Kunsch
; Patrick J. Dillon
; Steven Barash

TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14

ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 334:
SEQUENCE CHARACTERISTICS:
LENGTH: 9212 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Query Match 83.3%; Score 15; DB 9; Length 9212;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGGTTC 16
DB 4989 GTTAATTCGGTTC 5003

RESULT 13

US-09-535-459-1371/c
; Sequence 1371, Application US/09535459
; Publication No. US20030040615A1

GENERAL INFORMATION:

APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleageane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULES

FILE REFERENCE: PD-1014 CIP
CURRENT APPLICATION NUMBER: US/09/535,459
CURRENT FILING DATE: 2000-03-24
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2170
SOFTWARE: PERL Program
SEQ ID NO 1371
LENGTH: 262

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01153717
US-09-535-459-1371

Query Match 82.2%; Score 14.8; DB 10; Length 262;
Best Local Similarity 88.9%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCCGGTTCCTC 18
DB 102 CTTTAATTCCTTCCTC 85

RESULT 14

US-10-424-599-43896
; Sequence 43896, Application US/10424599
; Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 43896
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:

OTHER INFORMATION: Clone ID: PAT_MPT3847_139637C.1
US-10-424-599-43896

Query Match 82.2%; Score 14.8; DB 18; Length 438;
Best Local Similarity 88.9%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCCGGTTCCTC 18
DB 297 CGTTAATTCCGGTTCATC 314

RESULT 15

US-10-363-345A-1073
; Sequence 1073, Application US/10363345A
; Publication No. US20040234960A1

GENERAL INFORMATION:

APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined

; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3'
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 1073
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 1073
US-10-363-345A-1073

Query Match 82.2%; Score 14.8; DB 20; Length 554;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGTTAATTTCGCGTTCTTC 18
|||
Db 113 CGTTAATTTCGCGTTTATC 130
|||

Search completed: October 23, 2005, 23:48:19
Job time : 79.8251 secs

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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 06:56:31 ; Search time 12.5204 Seconds
(without alignments)
2744.464 Million cell updates/sec

Title: US-10-046-955-51
Perfect score: 21
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	US-09-423-233-51	Sequence 51, Appl
2	21	100.0	319	US-09-423-233-6	Sequence 6, Appl
3	19	90.5	561	US-08-905-314A-24	Sequence 24, Appl
C 4	16.2	77.1	601	US-09-949-016-87133	Sequence 87133, A
C 5	16.2	77.1	601	US-09-949-016-87134	Sequence 87134, A
C 6	16.2	77.1	33769	US-09-544-398B-8	Sequence 8, Appl
C 7	16.2	77.1	33769	US-09-543-771B-8	Sequence 8, Appl
C 8	16.2	77.1	89625	US-09-949-016-17012	Sequence 17012, A
C 9	16.2	77.1	140844	US-09-949-016-14199	Sequence 14199, A
C 10	15.4	73.3	2034	US-09-815-923-11	Sequence 11, Appl
C 11	15.4	73.3	29555	US-08-956-171E-206	Sequence 206, App
C 12	15.4	73.3	29555	US-08-781-986A-206	Sequence 206, App
C 13	15.4	73.3	36181	US-08-311-731A-120	Sequence 120, App
C 14	15.4	73.3	38494	US-08-311-731A-24	Sequence 24, Appl
C 15	15.4	73.3	38675	US-08-311-731A-135	Sequence 135, App
C 16	15.2	72.4	601	US-09-949-016-145735	Sequence 145735, A
C 17	15.2	72.4	601	US-09-949-016-146003	Sequence 146003, A
C 18	15.2	72.4	601	US-09-949-016-146271	Sequence 146271, A
C 19	15.2	72.4	601	US-09-949-016-150850	Sequence 150850, A
C 20	15.2	72.4	1173	US-09-398-858-13	Sequence 13, Appl
C 21	15.2	72.4	8207	US-09-902-540-925	Sequence 925, App
C 22	15.2	72.4	56963	US-09-949-016-12966	Sequence 12966, A
C 23	15.2	72.4	56968	US-09-949-016-11888	Sequence 11888, A
C 24	15.2	72.4	76124	US-09-949-016-11876	Sequence 11876, A
C 25	15.2	72.4	205044	US-09-949-016-15851	Sequence 15851, A
C 26	15.2	72.4	205044	US-09-949-016-15852	Sequence 15852, A
C 27	15.2	72.4	205044	US-09-949-016-15853	Sequence 15853, A

C 28	15.2	72.4	223471	4	US-09-949-016-12387	Sequence 12387, A
C 29	15.2	72.4	223471	4	US-09-949-016-12724	Sequence 12724, A
C 30	15.2	72.4	223471	4	US-09-949-016-13725	Sequence 12725, A
C 31	14.8	70.5	283	4	US-09-270-767-2818	Sequence 2818, Ap
C 32	14.8	70.5	283	4	US-09-270-767-18100	Sequence 18100, A
C 33	14.8	70.5	927	4	US-09-252-991A-5522	Sequence 5522, Ap
C 34	14.8	70.5	41171	4	US-08-311-731A-122	Sequence 122, App
C 35	14.8	70.5	42246	4	US-09-949-016-17008	Sequence 17008, A
C 36	14.8	70.5	53562	4	US-09-949-016-16286	Sequence 16286, A
C 37	14.8	70.5	59123	4	US-09-949-016-12177	Sequence 12177, A
C 38	14.8	70.5	83617	4	US-09-949-016-12254	Sequence 12254, A
C 39	14.8	70.5	1230025	4	US-09-198-452A-1	Sequence 1, Appli
C 40	14.8	70.5	1230230	4	US-09-438-185A-1	Sequence 1, Appli
C 41	14.8	70.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 42	14.8	70.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 43	14.6	69.5	25	4	US-09-396-196G-38445	Sequence 38445, A
C 44	14.6	69.5	25	4	US-09-396-196G-38446	Sequence 38446, A
C 45	14.6	69.5	25	4	US-09-396-196G-38447	Sequence 38447, A

ALIGNMENTS

RESULT 1
US-09-423-233-51
; Sequence 51, Application US/09423233
; Patent No. 6372430
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 03063-0341WP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Fusarium solani
US-09-423-233-51

Query Match 100.0%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACACCTCGCACTGGAGA 21
Db 1 CTAACACCTCGCACTGGAGA 21

RESULT 2
US-09-423-233-6
; Sequence 6, Application US/09423233
; Patent No. 6372430
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 03063-0341WP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
US-09-423-233-6

Query Match 100.0%; Score 21; DB 3; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACACCTCGCAACTGGAGA 21
|||||
Db 222 CTAACACCTCGCAACTGGAGA 242
|||||

RESULT 3
US-08-905-314A-24
; Sequence 24, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827695artis Corporation Patent Department
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Fusarium avenaceum
; INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /note= "3' end of small subunit
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..181
; OTHER INFORMATION: /note= "ITS 1"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 182..338
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 339..504
; OTHER INFORMATION: /note= "ITS 2"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 505..561
; OTHER INFORMATION: /note= "5' end of large subunit
; OTHER INFORMATION: rRNA gene"
US-08-905-314A-24

Query Match 90.5%; Score 19; DB 1; Length 561;

Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACACCTCGCAACTGGA 19
|||||
Db 445 CTAACACCTCGCAACTGGA 463
|||||

RESULT 4
US-09-949-016-87133/c
; Sequence 87133, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87133
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-87133

Query Match 77.1%; Score 16.2; DB 4; Length 601;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTAACACCTCGCAACTGGAGA 21
|||||
Db 483 CTAGCACCTCTCAACTGGACA 463
|||||

RESULT 5
US-09-949-016-87134/c
; Sequence 87134, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87134
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-87134

Query Match 77.1%; Score 16.2; DB 4; Length 601;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTAACACCTCGCAACTGGAGA 21
|||||

```
Db 66 CTAGCACCTCTCAACTGGACA 46

RESULT 6
US-09-544-398B-8
; Sequence 8, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 33769
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (33739), (33749), (33758)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknown
US-09-544-398B-8

Query Match 77.1%; Score 16.2; DB 4; Length 33769;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCAACTGGAGA 21
||| ||||| ||||| |||||
Db 25831 CTAGCACCTCTCAACTGGACA 25851

RESULT 7
US-09-543-771B-8
; Sequence 8, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US/09/543,771B
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 33769
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (33739), (33749), (33758)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknown
US-09-543-771B-8

Query Match 77.1%; Score 16.2; DB 4; Length 33769;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCAACTGGAGA 21
||| ||||| ||||| |||||
Db 25831 CTAGCACCTCTCAACTGGACA 25851

RESULT 8
US-09-949-016-17012/c
; Sequence 17012, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17012
; LENGTH: 89625
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)....(89625)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17012

Query Match 77.1%; Score 16.2; DB 4; Length 89625;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCAACTGGAGA 21
||| ||||| ||||| |||||
Db 32181 CTACCACCTCCCAAAATGGAGA 32161

RESULT 9
US-09-949-016-14199/c
; Sequence 14199, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14199
; LENGTH: 140844
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
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```

; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38675 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
; US-08-311-731A-135

Query Match      73.3%; Score 15.4; DB 4; Length 38675;
Best Local Similarity 94.1%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CACCTCGCACTGGAGA 21
      |||||
Db      3801 CACCTCGCACTGGCGA 3785

Search completed: October 23, 2005, 16:07:15
Job time : 19.5204 secs
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```
Query Match      100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.99; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy 1 CTAACACCTCGCAACTGGAGA 21
    |||||
Db 1 CTAACACCTCGCAACTGGAGA 21

RESULT 2
US-10-046-955-6
; Sequence 6, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Lilliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; PRIOR FILING DATE: 2002-06-04
; PRIOR FILING DATE: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
US-10-046-955-6

Query Match      100.0%; Score 21; DB 15; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy 1 CTAACACCTCGCAACTGGAGA 21
    |||||
Db 222 CTAACACCTCGCAACTGGAGA 242

RESULT 3
US-10-829-661-5
; Sequence 5, Application US/10829661
; Publication No. US20050009051A1
; GENERAL INFORMATION:
; APPLICANT: HAN XIANG-YANG
; APPLICANT: TARRAND, JEFFREY J.
; APPLICANT: PHAM, AUDREY S.
; APPLICANT: MAY, GREGORY S.
; TITLE OF INVENTION: DIAGNOSIS OF MOULD INFECTION
; FILE REFERENCE: UTSC865US
; CURRENT APPLICATION NUMBER: US/10/829,661
; PRIOR FILING DATE: 2004-04-21
; PRIOR APPLICATION NUMBER: 10/672,300
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/414,008
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Fusarium sp.
```

```
US-10-829-661-5

Query Match      90.5%; Score 19; DB 21; Length 552;
Best Local Similarity 100.0%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

Qy 1 CTAACACCTCGCAACTGGA 19
    |||||
Db 453 CTAACACCTCGCAACTGGA 471

RESULT 4
US-10-672-300-5
; Sequence 5, Application US/10672300
; Publication No. US20050048509A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: TARRAND, JEFFREY J.
; TITLE OF INVENTION: DIAGNOSIS OF INVASIVE MOLD INFECTION
; FILE REFERENCE: UTXC-766US
; CURRENT APPLICATION NUMBER: US/10/672,300
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/414,008
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Fusarium sp.
US-10-672-300-5

Query Match      90.5%; Score 19; DB 21; Length 552;
Best Local Similarity 100.0%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

Qy 1 CTAACACCTCGCAACTGGA 19
    |||||
Db 453 CTAACACCTCGCAACTGGA 471

RESULT 5
US-09-925-065A-367816/c
; Sequence 367816, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 367816
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-367816

Query Match      80.0%; Score 16.8; DB 12; Length 636;
Best Local Similarity 90.0%; Pred. No. 1.6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 18; Conservative 0;
```


QY 1 CTAACACCTCGCAACTGGAG 20
|||||
Db 230 CTAACACCTCTCAACTGGAG 211

RESULT 6
US-09-925-065A-367817/c
; Sequence 367817, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 367817
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-367817

Query Match 80.0%; Score 16.8; DB 12; Length 636;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCAACTGGAG 20
|||||
Db 230 CTAACACCTCTCAACTGGAG 211

RESULT 7
US-11-036-317-784700/c
; Sequence 784700, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE OF INVENTION: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 784700
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-784700

Query Match 77.1%; Score 16.2; DB 24; Length 25;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCAACTGGAG 21
|||||
Db 21 CCAACACCTGTAACTGGAG 1

RESULT 8
US-10-424-599-123319
; Sequence 123319, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 123319
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_82365C.1
US-10-424-599-123319

Query Match 77.1%; Score 16.2; DB 18; Length 403;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCAACTGGAG 21
|||||
Db 107 CTAACAGCACACACTGGAG 127

RESULT 9
US-10-027-632-136133
; Sequence 136133, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 136133
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-136133

Query Match 77.1%; Score 16.2; DB 13; Length 499;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCAACTGGAG 21
|||||
Db 55 CTAACCTCTCCCACTGGAG 75

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RESULT 10
US-10-027-632-136134
; Sequence 136134, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136134
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-136134

Query Match          77.1%; Score 16.2; DB 13; Length 499;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTAACACCTCGCAACTGGAGA 21
Db 55 CTAACCTCTCCCACTGGAGA 75

RESULT 11
US-10-027-632-136133
; Sequence 136133, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136133
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-136133

Query Match          77.1%; Score 16.2; DB 13; Length 499;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTAACACCTCGCAACTGGAGA 21
Db 55 CTAACCTCTCCCACTGGAGA 75

RESULT 12
US-10-027-632-136134
; Sequence 136134, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136134
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-136134

Query Match          77.1%; Score 16.2; DB 17; Length 499;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTAACACCTCGCAACTGGAGA 21
Db 55 CTAACCTCTCCCACTGGAGA 75

RESULT 13
US-09-925-065A-487968
; Sequence 487968, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
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